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OM protein - protein search, using sw model

Run on: August 9, 2004, 13:27:45 ; Search time 18 Seconds  
(without alignments)  
37.285 Million cell updates/sec

Title: US-09-277-074-9  
Perfect score: 74  
Sequence: 1 TPPAYRPPNAPIL 13

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/2/iaa/PTCTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	13	1	US-08-305-871A-14
2	74	100.0	13	4	US-08-464-496-19
3	74	100.0	13	4	US-08-788-822A-16
4	74	100.0	13	4	US-08-197-484-113
5	74	100.0	13	4	US-09-311-784A-49
6	74	100.0	13	4	US-09-664-945-50
7	74	100.0	13	5	PCT-US92-07218-19
8	74	100.0	13	5	PCT-US95-02121-113
9	74	100.0	13	5	PCT-US95-16415-9
10	74	100.0	14	4	US-09-311-784A-124
11	74	100.0	15	3	US-08-737-896-7
12	74	100.0	15	5	PCT-US96-09951-7
13	74	100.0	21	5	US-09-100-409A-45
14	74	100.0	21	5	PCT-US95-13841-13
15	74	100.0	23	4	US-08-464-496-20
16	74	100.0	23	4	US-08-197-484-114
17	74	100.0	23	5	PCT-US92-07218-20
18	74	100.0	23	5	PCT-US95-02121-114
19	74	100.0	26	4	US-08-464-496-21
20	74	100.0	26	4	US-08-197-484-115
21	74	100.0	26	5	PCT-US92-07218-21
22	74	100.0	26	5	PCT-US95-02121-115
23	74	100.0	80	4	US-09-311-784A-22
24	74	100.0	118	4	US-09-311-784A-8
25	74	100.0	119	4	US-09-311-784A-10
26	74	100.0	136	4	US-09-311-784A-12
27	74	100.0	138	4	US-09-311-784A-4

28	74	100.0	152	4	US-09-311-784A-20	Sequence 20, Appl
29	74	100.0	154	3	US-08-968-747-1	Sequence 1, Appl
30	74	100.0	155	3	US-08-968-747-17	Sequence 17, Appl
31	74	100.0	159	3	US-08-445-585-3	Sequence 3, Appl
32	74	100.0	161	3	US-08-968-747-19	Sequence 19, Appl
33	74	100.0	164	4	US-09-311-784A-18	Sequence 18, Appl
34	74	100.0	183	3	US-08-968-747-20	Sequence 20, Appl
35	74	100.0	183	3	US-09-248-588-2	Sequence 2, Appl
36	74	100.0	183	3	US-09-248-588-4	Sequence 4, Appl
37	74	100.0	183	5	PCT-US96-10602-12	Sequence 12, Appl
38	74	100.0	185	1	US-07-739-642-2	Sequence 2, Appl
39	74	100.0	185	1	US-07-739-642-4	Sequence 4, Appl
40	74	100.0	185	1	US-07-739-642-8	Sequence 8, Appl
41	74	100.0	185	1	US-07-739-642-10	Sequence 10, Appl
42	74	100.0	185	1	US-07-739-643-2	Sequence 2, Appl
43	74	100.0	185	1	US-07-739-643-4	Sequence 4, Appl
44	74	100.0	185	1	US-07-739-643-8	Sequence 8, Appl
45	74	100.0	185	1	US-07-739-643-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-08-305-871A-14  
; Sequence 14, Application US/08305871A  
; Patent No. 5736142  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Gaeta, Federico  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sidney, John  
; APPLICANT: Alexander, Jeffrey L.  
; TITLE OF INVENTION: Alteration of Immune Response Using Pan  
; TITLE OF INVENTION: DR-Binding Peptides  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/305,871A  
; FILING DATE: 14-SEP-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/121,101  
; FILING DATE: 14-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 14137-0062-10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-305-871A-14

Query Match 100.0%; Score 74; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
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Db 1 TPPAYRPPNAPIL 13

## RESULT 2

US-08-464-496-19  
; Sequence 19, Application US/08464496  
; Patent No. 6322789  
; GENERAL INFORMATION:  
; APPLICANT: Epimmune, Inc.  
; APPLICANT: Vitello, Maria  
; APPLICANT: Chesnut, Robert  
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL  
; TITLE OF INVENTION: EPITOPES  
; FILE REFERENCE: 39963-20001.13  
; CURRENT APPLICATION NUMBER: US/08/464,496  
; CURRENT FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: 07/935,811  
; PRIOR FILING DATE: 1992-08-26  
; PRIOR APPLICATION NUMBER: 07/874,491  
; PRIOR FILING DATE: 1992-04-27  
; PRIOR APPLICATION NUMBER: 07/827,682  
; PRIOR FILING DATE: 1992-01-29  
; PRIOR APPLICATION NUMBER: 07/749,568  
; PRIOR FILING DATE: 1991-08-26  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: T helper epitope HBC 128-140  
US-08-464-496-19

Query Match 100.0%; Score 74; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
|||||  
Db 1 TPPAYRPPNAPIL 13

## RESULT 3

US-08-788-822A-16  
; Sequence 16, Application US/08788822A  
; Patent No. 6413935  
; GENERAL INFORMATION:  
; APPLICANT: Alexander, Jeffrey L.  
; APPLICANT: Defrees, Shawn  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Induction of Immune Response Against  
; TITLE OF INVENTION: Desired Determinants  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/788,822A  
; FILING DATE: 23-JAN-1997

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/010,510  
FILING DATE: 24-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 014137-009210US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-788-822A-16

Query Match 100.0%; Score 74; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
|||||  
Db 1 TPPAYRPPNAPIL 13

## RESULT 4

US-08-197-484-113  
; Sequence 113, Application US/08197484  
; Patent No. 6419931  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; APPLICANT: CHESTNUT, Robert W.  
; APPLICANT: SETTE, Alessandro D.  
; APPLICANT: CELIS, Esteban  
; APPLICANT: GRAY, Howard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; TITLE OF INVENTION: CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990



PCT-US92-07218-19

Query Match 100.0%; Score 74; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13  
Db 1 TPPAYRPPNAPIL 13

## RESULT 8

PCT-US95-02121-113  
; Sequence 113, Application PC/TUS9502121  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; NUMBER OF SEQUENCES: 153  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/02121  
; FILING DATE: 16-FEB-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/197,484  
; FILING DATE: 16-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
PCT-US95-02121-113

Query Match 100.0%; Score 74; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13  
Db 1 TPPAYRPPNAPIL 13

## RESULT 9

PCT-US95-16415-9  
; Sequence 9, Application PC/TUS9516415  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute

; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC  
; TITLE OF INVENTION: CYTOTOXIC T CELLS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute  
; STREET: 10666 North Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/16415  
; FILING DATE: 13-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/355,558  
; FILING DATE: 14-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Logan, April C.  
; REGISTRATION NUMBER: 33,950  
; REFERENCE/DOCKET NUMBER: 433.1PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 554-2937  
; TELEFAX: (619) 554-6312  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US95-16415-9

Query Match 100.0%; Score 74; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13  
Db 1 TPPAYRPPNAPIL 13

## RESULT 10

US-09-311-784A-124  
; Sequence 124, Application US/09311784A  
; Patent No. 633482  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Eplimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.01  
; CURRENT APPLICATION NUMBER: US/09/311,784A  
; CURRENT FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 124  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HBVcore128

US-09-311-784A-124

Query Match 100.0%; Score 74; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13  
Db 1 TPPAYRPPNAPIL 13

RESULT 11

US-08-737-896-7

Sequence 7, Application US/08737896

Patent No. 6168804

GENERAL INFORMATION:

APPLICANT: Samuel, John

APPLICANT: Kwon, Glen S.

TITLE OF INVENTION: METHOD FOR ELICITING TH1-SPECIFIC

TITLE OF INVENTION: IMMUNE RESPONSE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/737,896

FILING DATE: 24-SEP-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/480,499

FILING DATE: 07-JUN-1996

APPLICATION NUMBER: PCT/US96/09551

FILING DATE: 07-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07254/037001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: Hbcag

US-08-737-896-7

Query Match 100.0%; Score 74; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13  
Db 3 TPPAYRPPNAPIL 15

RESULT 12

PCT-US96-09951-7

Sequence 7, Application PC/TUS9609951

GENERAL INFORMATION:

APPLICANT: The Governors of the University of Alberta

TITLE OF INVENTION: A METHOD FOR ELICITING A TH1-SPECIFIC

TITLE OF INVENTION: IMMUNE RESPONSE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: California

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/09951

FILING DATE: 06-JUN-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Learl, June M.

REGISTRATION NUMBER: 31,238

REFERENCE/DOCKET NUMBER: 07254/037WO1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 678-5070

TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: Hbcag

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..15

PCT-US96-09951-7

Query Match 100.0%; Score 74; DB 5; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.0002;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13  
Db 3 TPPAYRPPNAPIL 15

RESULT 13

US-09-100-409A-45

Sequence 45, Application US/09100409A

Patent No. 6090388

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: PEPTIDE COMPOSITION FOR

TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND

TITLE OF INVENTION: IMMUNE DISORDERS

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

SOFTWARE: #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/100,409A

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; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-409A-45
Query Match 100.0%; Score 74; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 9 TPPAYRPPNAPIL 21

RESULT 14
PCT-US95-13841-13
; Sequence 13, Application PC/TUS9513841
; GENERAL INFORMATION:
; APPLICANT: United Biomedical Inc; Walfield, Alan M.;
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Synthetic Ige Membrane Anchor
; TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13841
; FILING DATE: 25-OCT-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/328,519
; FILING DATE: 25-OCT-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin, Maria C.H.
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-13841-13
Query Match 100.0%; Score 74; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00028;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 9 TPPAYRPPNAPIL 21

RESULT 15
US-08-464-496-20
; Sequence 20, Application US/08464496
; Patent No. 6322789
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: Vitello, Maria
; APPLICANT: Chesnut, Robert
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; TITLE OF INVENTION: EPITOPES
; FILE REFERENCE: 39963-20001.13
; CURRENT APPLICATION NUMBER: US/08/464,496
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 07/935,811
; PRIOR FILING DATE: 1992-08-26
; PRIOR APPLICATION NUMBER: 07/874,491
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/827,682
; PRIOR FILING DATE: 1992-01-29
; PRIOR APPLICATION NUMBER: 07/749,568
; PRIOR FILING DATE: 1991-08-26
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T helper epitope HBC 128-140
US-08-464-496-20

Query Match 100.0%; Score 74; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

Search completed: August 9, 2004, 13:29:48
Job time : 19 secs
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Query Match      100.0%; Score 74; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TPPAYRPPNAPIL 13  
 DB 1 TPPAYRPPNAPIL 13

RESULT 2  
 AAR78929  
 ID AAR78929 standard; peptide; 13 AA.  
 XX AC AAR78929;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 27-MAR-1996 (first entry)  
 XX DE HBC 128-140 cytotoxic T lymphocyte epitope.  
 XX KW HBC 128-140; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte;  
 XX KW antigens; treatment; disease prevention; hepatitis B.  
 XX OS Hepatitis B virus.  
 XX PN WO9522317-A1.  
 XX PD 24-AUG-1995.  
 XX PF 16-FEB-1995; 95WO-US002121.  
 XX PR 16-FEB-1994; 94US-00197484.  
 XX PA (CYTE-) CYTEL CORP.  
 XX PI Vitello MA, Chesnut RW, Sette AD, Cellis E, Grey H;  
 XX DR WPI; 1995-302545/39.  
 XX PT Compn. inducing cytotoxic T lymphocyte response to pref. viral,  
 XX PT bacterial, parasitic or tumour antigens - useful in the treatment and  
 XX PT prevention of diseases associated with the antigen e.g. hepatitis B.  
 XX PS Example 4; Page 52; 109pp; English.  
 XX CC A compn. which induces a cytotoxic T lymphocyte (CTL) response to a  
 XX CC hepatitis B virus (HBV) antigen (Ag) in a mammal comprises, a HBV CTL Ag  
 XX CC response inducing peptide (i.e. AAR78929) and a lipid conjugated helper T  
 XX CC cell inducing peptide. The compn. is useful in the treatment and  
 XX CC prevention of hepatitis B. (Updated on 25-MAR-2003 to correct PI field.)  
 XX SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. NO. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 DB 1 TPPAYRPPNAPIL 13

RESULT 3  
 AAW39439  
 ID AAW39439 standard; peptide; 13 AA.  
 XX AC AAW39439;  
 XX DT 11-JUN-1998 (first entry)  
 XX DE Mouse H-2 I-Ab-restricted HBV core antigen-derived T helper epitope.  
 XX KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;  
 XX KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;  
 XX KW disease; anti-tumour; anti-viral.  
 XX PA (CYTE-) CYTEL CORP.

OS Synthetic.  
 OS Mus sp.  
 XX WO9741440-A1.  
 XX PD 06-NOV-1997.  
 XX PF 28-APR-1997; 97WO-NL000229.  
 XX PR 26-APR-1996; 96EP-00201145.  
 XX PR 23-DEC-1996; 96EP-00203670.  
 XX PA (UYLE-) RIJKSUNIV LEIDEN.  
 XX PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.  
 XX PI Van Der Burg SH, Kast WM, Toes REM, Offringa R, Melief CJM;  
 XX WPI; 1997-549891/50.  
 XX PT Method of selecting T cell peptide epitope(s) - by measuring the  
 XX PT stability of HLA class I-peptide complexes on intact B cells.  
 XX PS Example 2; Page 21; 109pp; English.  
 XX CC Peptides AAW39430-W39734 are used in a novel method for the selection of  
 XX CC immunogenic T-cell peptide epitopes present in polypeptide antigens.  
 XX CC Peptide AAW39439 is a mouse H-2 I-Ab restricted HBV core antigen-derived  
 XX CC T helper epitope which is injected into HLA-A\*0201Kb transgenic mice. The  
 XX CC method involves the identification of peptide sequences capable of  
 XX CC binding to an HLA (human leukocyte antigen) class I molecule and  
 XX CC measuring the binding of this epitope peptide to the HLA class I peptide.  
 XX CC The stability of binding of the peptide and MHC (major histocompatibility  
 XX CC complex) class I molecule is measured on intact human B cells carrying  
 XX CC the MHC molecule at their cell surfaces. The method can be used to select  
 XX CC peptide epitopes for generating vaccines against a disease associated  
 XX CC with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are  
 XX CC especially T-cell peptide epitopes with strong anti-tumour and anti-viral  
 XX CC immune responses  
 XX SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. NO. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 DB 1 TPPAYRPPNAPIL 13

RESULT 4  
 AAW50117  
 ID AAW50117 standard; peptide; 13 AA.  
 XX AC AAW50117;  
 XX DT 30-JUN-1998 (first entry)  
 XX DE Pan DR binding peptide (14).  
 XX KW Pan DR binding peptide; antigen binding site; MHC molecule; DR locus.  
 XX OS Synthetic.  
 XX PN US5736142-A.  
 XX PD 07-APR-1998.  
 XX PF 14-SEP-1994; 94US-00305871.  
 XX PR 14-SEP-1993; 93US-00121101.  
 XX PA (CYTE-) CYTEL CORP.



XX Sidney J, Sette A, Alexander JL, Gaeta F, Grey HM;  
PI WPI; 1998-239154/21.  
DR  
XX  
XX Peptides that bind to MHC molecules of all DR alleles - inhibiting or  
PT inducing MHC Class II mediated activation of T cells.  
XX  
XX Example 5; Col 35-36; 29pp; English.  
XX  
XX The present sequence, a pan DR binding peptide, is capable of binding  
CC antigen binding sites on MHC molecules, which are encoded by most of the  
CC alleles of a DR locus. The peptide can be used to inhibit or induce MHC  
CC Class II mediated activation of T-cells or helper T-cells, which  
CC themselves mediate a CTL response. The peptide can be used in mammals,  
CC especially humans, to inhibit T-cell-mediated events involved in  
CC allograft rejection, allergic responses and autoimmunity and as a vaccine  
CC adjuvant for enhancing an immune response against an administered  
CC immunogen. The peptide can be used with other immunogens to treat, e.g.  
CC prostate cancer, hepatitis B, hepatitis C, AIDS, renal and cervical  
CC carcinoma, lymphoma, CMV and condylyoma acuminatum  
XX  
XX Sequence 13 AA;  
Query Match 100.0%; Score 74; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TPPAYRPPNAPIL 13  
DB 1 TPPAYRPPNAPIL 13  
RESULT 5  
AAY52556  
ID AAY52556 standard; peptide; 13 AA.  
XX  
XX AC AAY52556;  
XX  
XX 06-AUG-2003 (revised)  
DT 28-FEB-2000 (first entry)  
XX  
XX HBV core antigen MHC class II epitope, encoded by I80T fusion gene.  
XX  
XX Chimeric; pan DR epitope; expression vector; promoter;  
KW major histocompatibility complex; MHC; targeting; peptide; epitope;  
KW antigen; presentation; class I; cytosolic pathway; endoplasmic reticulum;  
KW class II; extracellular antigen; endocytic pathway; helper T lymphocyte;  
KW HTL; universal epitope; cytotoxic T lymphocyte; CTL; immune response;  
KW immunogenicity; assay; vaccine; immunity; infection; pathogen; virus;  
KW HIV; HBV; HCV; hepatitis B; hepatitis C; bacterium; protozoan;  
KW tumour cell; autoimmune disease; activation; antiviral; antimalarial;  
KW immunoprotective; core antigen.  
XX  
XX Synthetic.  
OS Hepatitis B virus.  
XX  
XX WO9958658-A2.  
PN  
XX 18-NOV-1999.  
PD  
XX 13-MAY-1999; 98WO-US010646.  
XX  
XX 13-MAY-1998; 98US-00078904.  
PR  
XX 15-MAY-1998; 98US-0085751P.  
PR  
XX (EPIM-) EPIMUNE INC.  
PA  
XX Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;  
PI Chesnut RW;  
XX  
XX WPI; 2000-039103/03.  
XX

PT Expression vectors encoding major histocompatibility targeting sequence,  
XX used as, e.g. tumor vaccines.  
XX  
XX Example 1; Page 36; 130pp; English.  
XX  
XX This sequence represents a hepatitis B virus (HBV) core antigen MHC class  
CC II epitope, encoded by the I80T fusion gene (AA238617), used in an  
CC exemplification of the present invention. The invention relates to a  
CC novel expression vector comprising a promoter operably linked to a fusion  
CC gene encoding a major histocompatibility complex (MHC) targeting  
CC sequence, and two or more heterologous peptide epitopes. The MHC  
CC targeting sequence may be a class I targeting sequence, which directs  
CC an MHC class I epitope to a cytosolic pathway or to the endoplasmic  
CC reticulum, or an MHC class II targeting sequence, which directs  
CC extracellular antigens to enter the endocytic pathway to be processed  
CC into antigen peptides for presentation on MHC class II molecules. The  
CC heterologous epitopes may comprise either helper T lymphocyte (HTL)  
CC epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL  
CC epitope such as a pan DR epitope (PADRE). The vectors are useful for  
CC stimulating an immune response in vivo, as well as for use in assaying  
CC the human immunogenicity of a human T cell peptide epitope in vivo in a  
CC non-human mammal. They provide a nucleic acid vaccine for enhancing  
CC immunity against infectious pathogens, such as viruses (e.g., HIV,  
CC hepatitis B (HBV) and hepatitis C (HCV)), bacteria, protozoa (e.g.,  
CC Plasmodium falciparum, the cause of malaria) and also tumour cells and  
CC autoimmune diseases. Universal MHC class I and class II epitopes are advantageously  
CC combined with other MHC class I and class II epitopes to increase the  
CC number of cells that are activated in response to a given antigen and  
CC provide a broader population coverage of MHC-reactive alleles. (Updated  
CC on 06-AUG-2003 to correct OS field.)  
XX  
XX Sequence 13 AA;  
Query Match 100.0%; Score 74; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TPPAYRPPNAPIL 13  
DB 1 TPPAYRPPNAPIL 13  
RESULT 6  
AAG64542  
ID AAG64542 standard; peptide; 13 AA.  
XX  
XX AC AAG64542;  
XX  
XX 22-OCT-2001 (first entry)  
DT  
XX T-helper epitope peptide.  
DE  
XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;  
KW human immunodeficiency virus; vaccine; T-helper.  
XX  
XX Synthetic.  
OS  
XX WO200155177-A2.  
PN  
XX 02-AUG-2001.  
PD  
XX 29-JAN-2001; 2001WO-DK000059.  
XX  
XX 28-JAN-2000; 2000EP-00610017.  
PR  
XX 31-JAN-2000; 2000US-0179333P.  
PR  
XX (STAT-) STATENS SERUM INST.  
PA  
XX Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;  
PI WPI; 2001-476184/51.  
XX  
XX The generation of cytotoxic T cell lymphocytes epitopes for use in anti-  
PT

PT HIV vaccines.

XX Example 7; Page 42; 383pp; English.

PS The invention relates to identification of cytotoxic T cell lymphocyte

XX (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL

CC are a major protective mechanism against viral diseases. Antibodies may

CC neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine,

CC in the manufacture of vaccines or diagnostic agents. The present sequence

XX is that of a T-helper epitope peptide useful to the invention

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13

DB 1 TPPAYRPPNPAPIL 13

RESULT 7

AAE02681

ID AAE02681 standard; peptide; 13 AA.

AC AAE02681;

XX 06-AUG-2001 (first entry)

DT Hepatitis B virus HBVC helper peptide.

DE Cytostatic; antibacterial; antifungal; gene therapy; vaccine; antiviral;

XX tumour; epitope; glycoprotein; hepatitis B virus; HBV; immune response;

KW CTL; cytotoxic T lymphocyte; HLA; human leucocyte antigen.

OS Hepatitis B virus.

XX WO200127291-A1.

PN 19-APR-2001.

PD 29-SEP-2000; 2000WO-EP009902.

XX 12-OCT-1999; 99US-0158356P.

PR (INSP ) INST PASTEUR.

XX Firat H, Lemonnier F, Langlade-Demoyen P;

XX WPI; 2001-282038/29.

DR New polynucleotide comprising at least one viral, fungal, bacterial, or

PT tumour epitope of an antigen, capable of inducing a cellular response.

XX Example 1; Page 23; 70pp; English.

PS The invention relates to polynucleotide containing at least a part of the

CC coding sequence of the middle glycoprotein of hepatitis B virus (HBV) in

CC which is inserted a DNA sequence coding for an epitope comprising at

CC least one viral, fungal, bacterial, or tumour epitope of an antigen,

CC capable of inducing a cellular response. Nucleic acids and compositions

CC of the invention are useful for inducing in vivo a CTL (cytotoxic T

CC lymphocyte) response against several epitopes of one or more, bacterial,

CC viral, fungal, or tumour antigens. A composition of the invention

CC produces an immune response against HIV antigen and are used in the

CC production of vaccines. The polynucleotides of the invention are also

CC used in gene therapy. The present sequence is hepatitis B virus helper

CC peptide. This peptide is co-injected with human epitopes in order to

CC elicit HLA (human leucocyte antigen) -A2.1-restricted CTL response in

XX mice

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13

DB 1 TPPAYRPPNPAPIL 13

RESULT 8

AAE00471

ID AAE00471 standard; peptide; 13 AA.

XX AC AAE00471;

XX 19-JUN-2001 (first entry)

DT Hepatitis B virus core (HBVc) tumour epitopic peptide.

DE Tumour epitope; cytostatic; immunostimulant; gene therapy;

XX middle glycoprotein; Hepatitis B virus core; cytotoxic response;

KW immune response; cytotoxic T lymphocyte; CTL; HBVc; HLA;

XX human leucocyte antigen.

OS Hepatitis B virus.

XX WO200123577-A2.

PN 05-APR-2001.

PD 29-SEP-2000; 2000WO-EP009900.

XX 30-SEP-1999; 99US-0156945P.

PR (INSP ) INST PASTEUR.

XX Firat H, Lemonnier F, Langlade-Demoyen P, Michel M, Suhrbier AA;

XX WPI; 2001-266164/27.

DR Novel polynucleotide having DNA sequence encoding tumor antigen epitope

PT inserted in part of coding sequence of middle glycoprotein of hepatitis B

PT virus, used to induce immune response against tumor-specific antigen.

XX Example 1; Page 13; 36pp; English.

PS The present invention relates to an isolated or purified polynucleotide

XX containing a DNA sequence coding for at least one tumour epitope of a

CC tumour antigen inserted into part of the coding sequence of the middle

CC glycoprotein of the Hepatitis B virus (HBV). The polynucleotide is useful

CC for optionally evaluating cytotoxic responses in the individual's

CC lymphocyte population. It induces an immune response against at least one

CC tumour specific antigen or tissue specific antigen. The vector comprising

CC the polynucleotide induces in vivo, cellular and/or humoral immune

CC response. The composition comprising the polynucleotide induces in vivo,

CC cytotoxic T lymphocyte (CTL) against one or more antigens or epitopes

CC present on the hybrid protein. The polynucleotide is also useful in gene

CC therapy. The present sequence is a Hepatitis B virus core (HBVc) tumour

CC epitopic peptide. This peptide elicits HLA (human leucocyte antigen)-A2.1

CC -restricted CTL response in mice

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13

DB 1 TPPAYRPPNPAPIL 13

XX Hepatitis B core antigen peptide.  
DE  
XX  
XX Telomerase reverse transcriptase; hTERT; human; cytotoxic T lymphocyte;  
KW major histocompatibility complex; cancer; tumour;  
KW human leucocyte antigen; HLA-A2.1; HBVc; vaccine.  
XX  
XX  
OS Hepatitis B virus.  
XX  
XX WO200160391-A1.  
PN  
XX  
XX 23-AUG-2001.  
PD  
XX  
XX 15-FEB-2001; 2001WO-US005143.  
PF  
XX  
XX 15-FEB-2000; 2000US-0182685P.  
PR  
XX  
XX 15-FEB-2001; 2001US-00182685.  
PR  
XX  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX  
XX Zanetti M;  
PI  
XX  
XX WPI; 2001-536552/59.  
DR  
XX  
XX Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,  
PT for treating cancers or tumors or for inducing immune response against  
PT tumors, comprises a telomerase reverse transcriptase peptide.  
XX  
XX Example 1; Page 12; 52pp; English.  
PS  
XX  
XX The present sequence is that of a hepatitis B virus core antigen (HBVc)  
CC peptide comprising amino acid residues 128-140. The peptide was used to  
CC immunise HHD mice and results were compared with those obtained using  
CC human telomerase reverse transcriptase (hTERT) HLA-A2.1+ restricted  
CC peptide p540 (see AAB82772). The induction of CTL responses in vitro and  
CC in vivo, and the susceptibility to lysis of tumour cells of various  
CC origins by hTERT CTL suggest that hTERT could serve as a universal cancer  
CC vaccine for humans. A claimed universal vaccine for treating tumours of  
CC any origin comprises at least 1 hTERT peptide. The peptide is 7-15 amino  
CC acid residues in length and may be modified to enhance binding to the  
CC major histocompatibility complex. Also claimed is a method for inducing  
CC and enhancing a CTL response against cancer cells, involving harvesting  
CC blood leucocytes, pulsing with hTERT, and contacting cancer cells with the  
CC pulsed leucocytes. A method for targeting CTL to tumour cells is also  
CC claimed, and involves administering a hTERT peptide to a mammal,  
CC especially a cancer patient. (Updated on 06-AUG-2003 to correct OS  
XX field.)  
SQ Sequence 13 AA;  
Query Match 100.0%; Score 74; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TPPAYRPPNPAPIL 13  
DB 1 TPPAYRPPNPAPIL 13  
RESULT 11  
AAU00614  
ID AAU00614 standard; peptide; 13 AA.  
XX  
XX AAU00614;  
AC  
XX  
XX 12-SEP-2001 (first entry)  
DT  
XX  
XX H-2 I-Ab-restricted HBV core antigen-derived T helper epitope.  
DE  
XX  
XX Human; MUC1; antigenic peptide; major histocompatibility complex; MHC-I;  
KW glycoprotein; cytotoxic T lymphocytes; T cell response; cancer; vaccine;  
KW cancer gene therapy; diagnosis; treatment; inflammatory disorder; HBV;  
KW organ transplant rejection; graft versus host disease.  
XX

XX  
DE  
XX  
XX AAG62426 standard; peptide; 13 AA.  
KW  
XX  
XX AAG62426;  
AC  
XX  
XX 03-SEP-2001 (first entry)  
DT  
XX  
XX Immunogenic peptide HBV core SEQ ID 30.  
DE  
XX  
XX Class I epitope; immunogenic; heteroclitic analogue; immune response;  
KW antigen display; viral disease; cancer.  
KW  
XX  
XX Synthetic.  
OS  
XX  
XX WO200136452-A2.  
PN  
XX  
XX 25-MAY-2001.  
PD  
XX  
XX 20-NOV-2000; 2000WO-US031856.  
PF  
XX  
XX 18-NOV-1999; 99US-0166529P.  
PR  
XX  
XX 06-OCT-2000; 2000US-0239008P.  
PR  
XX  
XX (EPIM-) EPIMUNE INC.  
PA  
XX  
XX Tangri S, Sette A, Ishioka G;  
PI  
XX  
XX WPI; 2001-355609/37.  
DR  
XX  
XX Enhancing immunogenicity of peptide containing class I epitope, useful  
PT for treating cancer, comprises providing (semi-)conservative amino acid  
PT substitutions at specified positions of these epitopes.  
PT  
XX  
XX Disclosure; Fig 1A; 96pp; English.  
PS  
XX  
XX This invention relates to a method of enhancing the immunogenicity of a  
CC peptide, where the peptide contains a class I epitope. The invention  
CC includes methods for preparing peptides containing epitopes which have  
CC enhanced ability to effect an immune response (compared to wild-type  
CC epitopes). The peptides are referred to as heteroclitic analogues. The  
CC method is useful for eliciting an immune response by contacting CTLs with  
CC the immunogenically enhanced peptide in vitro in the presence of an  
CC antigen presenting cell, or by administering to a subject a nucleic acid  
CC molecule comprising a nucleotide sequence encoding the peptide. The  
CC peptides are useful as reagents to evaluate an immune response and the  
CC efficacy of the vaccine, and for making antibodies. The heteroclitic  
CC analogues are useful in immunological compositions for the treatment of  
CC viral diseases, cancer, and other conditions which are characterised by  
CC displayed antigens on target cells. The present sequence represents a  
CC class I epitope which may be used in the method of the invention  
XX  
SQ Sequence 13 AA;  
Query Match 100.0%; Score 74; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TPPAYRPPNPAPIL 13  
DB 1 TPPAYRPPNPAPIL 13  
RESULT 10  
AAB82775  
ID AAB82775 standard; protein; 13 AA.  
XX  
XX AAB82775;  
AC  
XX  
XX 06-AUG-2003 (revised)  
DT  
XX  
XX 29-OCT-2001 (first entry)  
DT



PF 21-JUL-2000; 2000FR-00009591.  
 XX  
 PR 21-JUL-2000; 2000FR-00009591.  
 XX  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA  
 XX Kosmatopoulos K, Tourdot S, Scardino A, Gross DA;  
 PI  
 XX WPI; 2002-189846/25.  
 DR  
 XX Identifying subdominant or cryptic epitopes, useful in immunotherapy of  
 PT cancer and viral infection, comprises testing modified, non-immunogenic  
 PT peptides for induction of cytotoxic T cells.  
 XX  
 XX Example 1; Page 14; 62pp; French.  
 PS  
 XX The present invention relates to subdominant/cryptic epitopes that are  
 CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The  
 CC epitopes or chimeric polypeptides containing them and nucleic acid  
 CC encoding them are useful for preventative or curative immunotherapy of  
 CC cancer and viral infections, particularly where used as vaccines. The  
 CC present peptide was used to illustrate the invention  
 XX  
 XX Sequence 13 AA;  
 SQ

Query Match 100.0%; Score 74; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TPPAYRPPNAPIL 13  
 Db 1 TPPAYRPPNAPIL 13  
 |||||

RESULT 14  
 ABP52344  
 ID ABG62860 standard; peptide; 13 AA.  
 XX  
 AC ABG62860;  
 XX  
 DT 21-AUG-2002 (first entry)  
 XX  
 DE Antigenic domain peptide from a Hepatitis B virus protein.  
 XX  
 KW Ligand/receptor specificity exchanger; antibody; pathogen receptor;  
 KW bacterial infection; viral infection; yeast infection; cancer;  
 KW parasitic infection; fungal infection; proliferation; antibacterial;  
 KW virucide; cytostatic; antifungal; antigenic domain.  
 XX  
 OS Hepatitis B virus.  
 XX  
 FN WO200224887-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 XX 19-SEP-2001; 2001WO-IB002327.  
 PF  
 XX 19-SEP-2000; 2000US-00664025.  
 PR  
 XX (TRIP-) TRIPER AB.  
 PA  
 XX Sallberg M, Flock J;  
 PI  
 XX WPI; 2002-499707/52.  
 DR  
 XX Novel ligand/receptor specificity exchanger that redirects antibodies to  
 PT receptors on pathogen or tumor cell, has specificity domain having ligand  
 PT for receptor, and antigenic domain having epitope of pathogen or toxin.  
 XX  
 XX Claim 14; Page 14; 79pp; English.  
 PS  
 XX The present invention relates to ligand/receptor specificity exchangers  
 CC comprising at least one specificity domain comprising a ligand for a

CC receptor, and at least one antigenic domain joined to the specificity  
 CC domain, where the antigenic domain comprises an epitope of a pathogen or  
 CC toxin. The ligand/receptor specificity exchangers redirect antibodies to  
 CC receptors present on pathogens. They are useful for preventing and  
 CC treating human diseases such as bacterial, viral, yeast, parasitic and  
 CC fungal infections, and cancer. These compositions act by inhibiting  
 CC proliferation of pathogens, or cancer cells. One of the prophylactic  
 CC applications of the ligand/receptor specificity exchangers includes  
 CC coating or crosslinking it to a medical device or implant which include  
 CC implantable medical devices that tend to serve as foci for infection by a  
 CC number of bacterial species. ABG62853-ABG62869 represent antigenic domain  
 CC peptides used in the methods of the present invention  
 XX  
 XX Sequence 13 AA;  
 SQ

Query Match 100.0%; Score 74; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TPPAYRPPNAPIL 13  
 Db 1 TPPAYRPPNAPIL 13  
 |||||

RESULT 15  
 ABP52344  
 ID ABP52344 standard; peptide; 13 AA.  
 XX  
 AC ABP52344;  
 XX  
 DT 17-OCT-2002 (first entry)  
 XX  
 DE TH epitope.  
 XX  
 KW Cytotoxic T lymphocyte; CTL; T helper; MAG3; cytotoxic T cell response;  
 KW tumour; immune response; cancer; vaccine; antibody.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200258728-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 XX 28-JAN-2002; 2002WO-GB000354.  
 PF  
 XX 26-JAN-2001; 2001GB-00002145.  
 PR  
 XX (SCRM-) SCANCELL LTD.  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 XX Durrant LG, Parsons T, Robins A;  
 PI  
 XX WPI; 2002-608418/55.  
 DR  
 XX Use of polypeptides and nucleic acids encoding the polypeptides, in  
 PT manufacturing medicament for stimulating a cytotoxic T cell response and  
 PT for preventing or treating cancer, e.g. colorectal, lung, breast or  
 PT ovarian cancer.  
 XX  
 XX Example 11; Page 45; 87pp; English.  
 PS  
 XX The present invention describes the use of a polypeptide (I) in the  
 CC manufacture of a medicament for stimulating a cytotoxic T cell response,  
 CC where (I) comprises a first portion comprising the part of human Fc that  
 CC binds to CD64 and a second portion comprising one or more heterologous T  
 CC cell epitopes. Also described is a method of stimulating a cytotoxic T  
 CC cell response in a patient such as a mammal, preferably human, by  
 CC administering (I) to the patient. (I) has cytostatic activity and can be  
 CC used in vaccine production. (I) and the nucleic acid encoding (I) are  
 CC useful in the manufacture of a medicament for stimulating cytotoxic T  
 CC cell response. The medicament is useful for preventing and/or treating  
 CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The  
 CC medicament stimulates cytotoxic and helper T cell responses. The

CC antibodies are useful as vaccines to stimulate helper and cytotoxic T  
CC cell responses. The polypeptides and nucleic acids are useful in  
CC optimising immunisation schedules for enhancing a protective immune  
CC response against cancer. The present sequence represents a TH epitope  
CC which is used in an example from the present invention

XX

SQ Sequence 13 AA;

Query Match . 100.0%; Score 74; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 1 TPPAYRPPNAPIL 13

Search completed: August 9, 2004, 13:27:41  
Job time : 53 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2004, 13:28:56 ; Search time 43 Seconds  
(without alignments)  
94.834 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74  
Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 31362936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	13	9	US-09-839-447A-86
2	74	100.0	13	10	US-09-277-074-9
3	74	100.0	13	12	US-09-277-064-9
4	74	100.0	13	12	US-10-371-525-49
5	74	100.0	13	12	US-10-372-735-55
6	74	100.0	13	12	US-10-182-252A-1374
7	74	100.0	13	12	US-10-333-430-63
8	74	100.0	13	12	US-09-788-110A-4
9	74	100.0	13	12	US-09-055-744-10
10	74	100.0	13	12	US-10-106-487-22
11	74	100.0	13	14	US-10-128-711-113
12	74	100.0	13	14	US-10-116-118-30
13	74	100.0	13	15	US-10-371-069-49
14	74	100.0	13	15	US-10-371-645-49
15	74	100.0	13	15	US-10-371-260-49

16	74	100.0	13	15	US-10-369-060A-86
17	74	100.0	13	15	US-10-388-337-22
18	74	100.0	13	15	US-10-608-541-50
19	74	100.0	14	12	US-10-371-525-124
20	74	100.0	14	15	US-10-371-069-124
21	74	100.0	14	15	US-10-371-645-124
22	74	100.0	14	15	US-10-371-260-124
23	74	100.0	16	14	US-10-106-876-3
24	74	100.0	18	14	US-10-106-876-10
25	74	100.0	20	9	US-09-839-447A-107
26	74	100.0	20	15	US-10-369-060A-107
27	74	100.0	21	8	US-08-785-997-43
28	74	100.0	21	10	US-09-387-340-43
29	74	100.0	21	10	US-09-386-591-43
30	74	100.0	23	14	US-10-128-711-114
31	74	100.0	26	14	US-10-128-711-115
32	74	100.0	80	12	US-10-371-525-22
33	74	100.0	80	15	US-10-371-069-22
34	74	100.0	80	15	US-10-371-645-22
35	74	100.0	80	15	US-10-371-260-22
36	74	100.0	118	12	US-10-371-525-8
37	74	100.0	118	15	US-10-371-069-8
38	74	100.0	118	15	US-10-371-645-8
39	74	100.0	118	15	US-10-371-260-8
40	74	100.0	119	12	US-10-371-525-10
41	74	100.0	119	15	US-10-371-069-10
42	74	100.0	119	15	US-10-371-645-10
43	74	100.0	119	15	US-10-371-260-10
44	74	100.0	136	12	US-10-371-525-12
45	74	100.0	136	15	US-10-371-069-12

ALIGNMENTS

RESULT 1  
US-09-839-447A-86  
; Sequence 86, Application US/09839447A  
; Patent No. US20020058247A1  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; FILE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS  
; FILE REFERENCE: TRIPEP 020CPI  
; CURRENT APPLICATION NUMBER: US/09/839,447A  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/556605  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-09-839-447A-86

Query Match 100.0%; Score 74; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
|||||  
DB 1 TPPAYRPPNAPIL 13

RESULT 2  
US-09-277-074-9  
; Sequence 9, Application US/09277074  
; Publication No. US2003002820A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, Linda A.

```
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR2155S
; CURRENT APPLICATION NUMBER: US/09/277,074
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-277-074-9

Query Match      100.0%; Score 74; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 3
US-09-277-064-9
; Sequence 9, Application US/09277064
; Publication No. US20030064916A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR2152S
; CURRENT APPLICATION NUMBER: US/09/277,064
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-277-064-9

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 4
US-10-371-525-49
; Sequence 49, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
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; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-525-49

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 5
US-10-372-735-55
; Sequence 55, Application US/10372735
; Publication No. US2003025251A1
; GENERAL INFORMATION:
; APPLICANT: Saliberg, Mattci
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; FILE REFERENCE: TRIPEP.7AUC4CP1
; CURRENT APPLICATION NUMBER: US/10/372,735
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/234,579
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-06
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE95/00468
; PRIOR FILING DATE: 1995-04-27
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/664,025
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: PCT/IB01/02327
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 10/153,271
; PRIOR FILING DATE: 2002-05-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptides
US-10-372-735-55

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13
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RESULT 6  
 US-10-182-252A-1374  
 ; Sequence 1374, Application US/10182252A  
 ; Publication No. US20040072162A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FOMSGAARD, ANDERS  
 ; APPLICANT: BRUNAK, SOREN  
 ; APPLICANT: BUUS, SOREN  
 ; APPLICANT: CORBET, SYLVIE  
 ; APPLICANT: LAUEMOLLER, SANNE LISE  
 ; APPLICANT: HANSEN, JAN  
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
 ; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
 ; FILE REFERENCE: 030307/0205  
 ; CURRENT APPLICATION NUMBER: US/10/182,252A  
 ; CURRENT FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
 ; PRIOR FILING DATE: 2001-01-29  
 ; PRIOR APPLICATION NUMBER: EP 00610017.6  
 ; PRIOR FILING DATE: 2000-01-28  
 ; PRIOR APPLICATION NUMBER: US 60/179,333  
 ; PRIOR FILING DATE: 2000-01-31  
 ; NUMBER OF SEQ ID NOS: 1388  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1374  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus  
 US-10-182-252A-1374

Query Match 100.0%; Score 74; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 DB 1 TPPAYRPPNAPIL 13

RESULT 7  
 US-10-333-430-63  
 ; Sequence 63, Application US/10333430  
 ; Publication No. US20040072240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INSERM  
 ; APPLICANT: INSTITUT GUSTAVE ROUSSY  
 ; APPLICANT: KOSMATOPOULOS, Kostas  
 ; APPLICANT: TOUDDOR, Sophie  
 ; APPLICANT: SCARDINO, Antonio  
 ; APPLICANT: GROSS, David, Alexandre  
 ; TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN  
 ; TITLE OF INVENTION: IMMUNOTHERAPY  
 ; FILE REFERENCE: 33339/259034  
 ; CURRENT APPLICATION NUMBER: US/10/333,430  
 ; CURRENT FILING DATE: 2003-10-02  
 ; PRIOR APPLICATION NUMBER: FR 0009591  
 ; PRIOR FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 70  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 63  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic peptide  
 US-10-333-430-63

Query Match 100.0%; Score 74; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

DB 1 TPPAYRPPNAPIL 13

RESULT 8  
 US-09-788-110A-4  
 ; Sequence 4, Application US/09788110A  
 ; Publication No. US20040086518A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zanetti, Maurizio  
 ; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing  
 ; TITLE OF INVENTION: Telomerase Reverse Transcriptase  
 ; FILE REFERENCE: UCSD-07017  
 ; CURRENT APPLICATION NUMBER: US/09/788,110A  
 ; CURRENT FILING DATE: 2001-02-15  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 4  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-788-110A-4

Query Match 100.0%; Score 74; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 DB 1 TPPAYRPPNAPIL 13

RESULT 9  
 US-09-055-744-10  
 ; Sequence 10, Application US/09055744  
 ; Publication No. US20010019714A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sia, Charles  
 ; APPLICANT: Chong, Pele  
 ; APPLICANT: Klein, Michel  
 ; TITLE OF INVENTION: HIV-SPECIFIC CYTOTONIX T-CELL RESPONSES  
 ; FILE REFERENCE: 1038-746  
 ; CURRENT APPLICATION NUMBER: US/09/055,744  
 ; CURRENT FILING DATE: 1998-04-07  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 US-09-055-744-10

Query Match 100.0%; Score 74; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 DB 1 TPPAYRPPNAPIL 13

RESULT 10  
 US-10-106-487-22  
 ; Sequence 22, Application US/10106487  
 ; Publication No. US20020164721A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FIRAT, HUSEYIN  
 ; APPLICANT: LEMONNIER, FRANCOIS  
 ; APPLICANT: LANGLADE-DEMOYEN, PIERRE  
 ; APPLICANT: MICHEL, MARIE-LOUISE  
 ; TITLE OF INVENTION: DESIGN OF A POLYPEPTIC CONSTRUCT FOR THE INDUCTION  
 ; TITLE OF INVENTION: OF  
 ; TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING

/ TITLE OF INVENTION: HHD MICE  
/ FILE REFERENCE: 03495.0196 SEQUENCE LISTING  
/ CURRENT APPLICATION NUMBER: US/10/106,487  
/ CURRENT FILING DATE: 2002-03-27  
/ PRIOR APPLICATION NUMBER: 09/675,673  
/ PRIOR FILING DATE: 2000-09-29  
/ PRIOR APPLICATION NUMBER: 60/158,356  
/ PRIOR FILING DATE: 1999-10-12  
/ NUMBER OF SEQ ID NOS: 41  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 22  
/ LENGTH: 13  
/ TYPE: PRI  
/ ORGANISM: Hepatitis B virus  
US-10-106-487-22

Query Match 100.0%; Score 74; DB 13; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
Db 1 TPPAYRPPNAPIL 13

RESULT 11  
US-10-128-711-113  
/ Sequence 113, Application US/10128711  
/ Publication No. US20030099634A1  
/ GENERAL INFORMATION:  
/ APPLICANT: VITIELLO, Maria A.  
/ CHESTNUT, Robert W.  
/ SETTE, Alessandro D.  
/ CELIS, Esteban  
/ GRAY, Howard  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
CTL IMMUNITY  
/ NUMBER OF SEQUENCES: 153  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend Khourie and Crew  
/ STREET: Stuart Street Tower, One Market Plaza  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: US  
/ ZIP: 94105-1493  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/10/128,711  
/ FILING DATE: 22-Apr-2002  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/197,484  
/ FILING DATE: 16-FEB-1994  
/ APPLICATION NUMBER: US 07/935,811  
/ FILING DATE: 26-AUG-1992  
/ APPLICATION NUMBER: US 07/874,491  
/ FILING DATE: 27-APR-1992  
/ APPLICATION NUMBER: US 07/827,682  
/ FILING DATE: 29-JAN-1992  
/ APPLICATION NUMBER: US 07/749,568  
/ FILING DATE: 26-AUG-1991  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Parmelee, Steven W.  
/ REGISTRATION NUMBER: 31,990  
/ REFERENCE/DOCKET NUMBER: 14137-26-4  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (206) 467-9600  
/ TELEFAX: (206) 623-6793  
/ INFORMATION FOR SEQ ID NO: 113:

/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 13 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: unknown  
/ TOPOLOGY: unknown  
/ MOLECULE TYPE: peptide  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 113:  
US-10-128-711-113

Query Match 100.0%; Score 74; DB 14; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
Db 1 TPPAYRPPNAPIL 13

RESULT 12  
US-10-116-118-30  
/ Sequence 30, Application US/10116118  
/ Publication No. US20030143672A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Tangri, Shabnam  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Ishioka, Glenn  
/ APPLICANT: Fikes, John D.  
/ TITLE OF INVENTION: Heterocyclic Analogs and Related Methods  
/ FILE REFERENCE: 2060.0090003  
/ CURRENT APPLICATION NUMBER: US/10/116,118  
/ CURRENT FILING DATE: 2002-08-07  
/ PRIOR APPLICATION NUMBER: US 60/166,529  
/ PRIOR FILING DATE: 1999-11-18  
/ PRIOR APPLICATION NUMBER: US 60/239,008  
/ PRIOR FILING DATE: 2000-10-06  
/ NUMBER OF SEQ ID NOS: 53  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 30  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: (HBV core)  
US-10-116-118-30

Query Match 100.0%; Score 74; DB 14; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
Db 1 TPPAYRPPNAPIL 13

RESULT 13  
US-10-371-069-49  
/ Sequence 49, Application US/10371069  
/ Publication No. US20030216342A1  
/ GENERAL INFORMATION:  
/ APPLICANT: EPIMMUNE Inc.  
/ APPLICANT: Fikes, John D.  
/ APPLICANT: Hermanson, Gary G.  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Ishioka, Glenn Y.  
/ APPLICANT: Livingston, Brian  
/ APPLICANT: Chesnut, Robert W.  
/ APPLICANT: Epimmune Inc.  
/ TITLE OF INVENTION: Expression Vectors for Stimulating an  
/ IMMUNE RESPONSE  
/ FILE REFERENCE: 39963-20022.10  
/ CURRENT APPLICATION NUMBER: US/10/371,069  
/ CURRENT FILING DATE: 2003-02-21  
/ PRIOR APPLICATION NUMBER: US 09/078,904

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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-069-49
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Query Match          100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TPPAYRPPNPAPIL 13
Db 1 TPPAYRPPNPAPIL 13
|||||
```

```
RESULT 14
US-10-371-645-49
; Sequence 49, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-645-49
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Query Match          100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TPPAYRPPNPAPIL 13
Db 1 TPPAYRPPNPAPIL 13
|||||
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RESULT 15
US-10-371-260-49
; Sequence 49, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
```

```
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-260-49
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Query Match          100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TPPAYRPPNPAPIL 13
Db 1 TPPAYRPPNPAPIL 13
|||||
```

```
Search completed: August 9, 2004, 13:34:25
Job time : 44 secs
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2004, 13:27:25 ; Search time 16 Seconds  
(without alignments)  
78.156 Million cell updates/sec

Title: US-09-277-074-9  
Perfect score: 74  
Sequence: 1 TPPAYRPPNAPIL 13  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR 78:\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	74	100.0	183	1 NKVLA2	core antigen - hep
2	74	100.0	183	1 NKVLCF	core antigen - hep
3	74	100.0	183	2 S3214	core antigen - hep
4	74	100.0	183	2 S3221	core antigen - hep
5	74	100.0	183	2 S3232	core antigen - hep
6	74	100.0	183	2 S3247	core antigen - hep
7	74	100.0	183	2 S3260	core antigen - hep
8	74	100.0	183	2 S3270	core antigen - hep
9	74	100.0	183	2 S3129	core antigen - hep
10	74	100.0	183	2 S3140	core antigen - hep
11	74	100.0	183	2 S3152	core antigen - hep
12	74	100.0	183	2 S3166	core antigen - hep
13	74	100.0	183	2 S3169	core antigen - hep
14	74	100.0	183	2 S3172	core antigen - hep
15	74	100.0	183	2 S3175	core antigen - hep
16	74	100.0	183	2 S3186	core antigen - hep
17	74	100.0	183	2 S3189	core antigen - hep
18	74	100.0	183	2 S3194	core antigen - hep
19	74	100.0	183	2 S3205	core antigen - hep
20	74	100.0	183	2 S20755	core antigen - hep
21	74	100.0	184	2 S3146	core antigen - hep
22	74	100.0	195	1 NKVLH3	core antigen - hep
23	74	100.0	211	1 NKVLA1	e antigen precursor
24	74	100.0	212	1 NKVLAH	e antigen precursor
25	74	100.0	212	1 NKVLA4	e antigen precursor
26	74	100.0	212	1 NKVLA4	e antigen precursor
27	74	100.0	212	1 NKVLJ1	e antigen precursor
28	74	100.0	212	1 NKVLJ2	e antigen precursor
29	74	100.0	212	2 S53211	e antigen precursor

30	74	100.0	212	2 S53216	e antigen precursor
31	74	100.0	212	2 S53223	e antigen precursor
32	74	100.0	212	2 S53225	e antigen precursor
33	74	100.0	212	2 S53229	e antigen precursor
34	74	100.0	212	2 S53236	e antigen precursor
35	74	100.0	212	2 S53238	e antigen precursor
36	74	100.0	212	2 S53240	e antigen precursor
37	74	100.0	212	2 S53242	e antigen precursor
38	74	100.0	212	2 S53251	e antigen precursor
39	74	100.0	212	2 S53253	e antigen precursor
40	74	100.0	212	2 S53255	e antigen precursor
41	74	100.0	212	2 S53257	e antigen precursor
42	74	100.0	212	2 S53272	e antigen precursor
43	74	100.0	212	2 S53274	e antigen precursor
44	74	100.0	212	2 S53279	e antigen precursor
45	74	100.0	212	2 S53281	e antigen precursor

ALIGNMENTS

RESULT 1  
NKVLA2  
Core antigen - hepatitis B virus (subtype adyw)  
C:Species: hepatitis B virus, HBV  
A:Variety: subtype adyw  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jul-1999  
C:Accession: B93217; A03711  
R:Pasek, M.; Goto, T.; Gilbert, W.; Zink, B.; Schaller, H.; MacKay, P.; Leadbetter, G.; Nature 282, 575-579, 1979  
A:Title: Hepatitis B virus genes and their expression in E. coli.  
A:Reference number: A93217; MUID:81012115; PMID:399329  
A:Accession: B93217  
A:Molecule type: DNA  
A:Residues: 1-183 <PAS>  
A:Cross-references: GB:J02202; NID:G329637; PIDN:AAA45486.1; PID:G329638  
A:Experimental source: subtype adyw  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor c  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein  
F:1-183/Product: core antigen #status predicted <MAT>

Query Match 100.0%; Score 74; DB 1; Length 183;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TPPAYRPPNAPIL 13  
Db 128 TPPAYRPPNAPIL 140

RESULT 2  
NKVLCF  
Core antigen - hepatitis B virus (strain LSH, chimpanzee)  
N:Alternate names: HBC antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: strain LSH, chimpanzee  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 16-Jun-2000  
C:Accession: A28885  
R:Vaadin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J. J. Gen. Virol. 69, 1383-1389, 1988  
A:Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated f  
A:Reference number: A92796; MUID:88258473; PMID:2838576  
A:Accession: A28885  
A:Molecule type: DNA  
A:Residues: 1-183 <VAU>  
A:Cross-references: EMBL:D00220; NID:G221505; PIDN:BAA00157.1; PID:G221506  
A:Experimental source: strain LSH, chimpanzee  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor c  
C:Genetics:  
A:Gene: C

C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 100.0%; Score 74; DB 1; Length 183;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
128 TPPAYRPPNAPIL 140  
|||||

Db 128 TPPAYRPPNAPIL 140

RESULT 3  
S53214  
core antigen - hepatitis B virus (isolate patient Castag-2'86)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Castag-2'86  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53214  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53214  
A:Molecule type: DNA  
A:Residues: 1-183 <LAI>  
A:Cross-references: EMBL:X85292; NID:g736120; PIDN:CAA59614.1; PID:g736123  
A:Experimental source: isolate patient Castag-2'86  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
128 TPPAYRPPNAPIL 140  
|||||

Db 128 TPPAYRPPNAPIL 140

RESULT 4  
S53221  
core antigen - hepatitis B virus (isolate patient Giulio'92)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Giulio'92  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53221  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53221  
A:Molecule type: DNA  
A:Residues: 1-183 <LAI>  
A:Cross-references: EMBL:X85258; NID:g736127; PIDN:CAA59525.1; PID:g736130  
A:Experimental source: isolate patient Giulio'92  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
128 TPPAYRPPNAPIL 140  
|||||

Db 128 TPPAYRPPNAPIL 140

RESULT 5  
S53232  
core antigen - hepatitis B virus (isolate patient Dettori-2'87)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Dettori-2'87  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53232  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53232  
A:Molecule type: DNA  
A:Residues: 1-183 <LAI>  
A:Cross-references: EMBL:X85299; NID:g736146; PIDN:CAA59623.1; PID:g736149  
A:Experimental source: isolate patient Dettori-2'87  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
128 TPPAYRPPNAPIL 140  
|||||

Db 128 TPPAYRPPNAPIL 140

RESULT 6  
S53247  
core antigen - hepatitis B virus (isolate patient Flore-2'91)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Flore-2'91  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53247  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53247  
A:Molecule type: DNA  
A:Residues: 1-183 <LAI>  
A:Cross-references: EMBL:X85305; NID:g736168; PIDN:CAA59642.1; PID:g736171  
A:Experimental source: isolate patient Flore-2'91  
A:Note: due to a stop codon between the alternative initiators the e antigen precursor  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
128 TPPAYRPPNAPIL 140  
|||||

Db 128 TPPAYRPPNAPIL 140

RESULT 7  
S53260  
core antigen - hepatitis B virus (isolate patient Mamoni-3'94)  
N:Alternate names: HBC antigen  
N:Contains: core antigen  
C:Species: hepatitis B virus, HBV

A;Variety: isolate patient Mannoni-3'94  
 C;Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
 C;Accession: S53260  
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A;Reference number: S53112  
 A;Accession: S53260  
 A;Molecule type: DNA  
 A;Residues: 1-183 <LAI>  
 A;Cross-references: EMBL:X85311; NID:g736187; PIDN:CAA59655.1; PID:g736190  
 A;Experimental source: isolate patient Mannoni-3'94  
 A;Note: due to a stop codon between the alternative initiators the e antigen precursor  
 C;Genetics:  
 A;Gene: C  
 C;Superfamily: hepatitis B virus core antigen  
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 0.00066;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 |||||  
 DB 128 TPPAYRPPNAPIL 140

RESULT 8  
 S53270  
 core antigen - hepatitis B virus (isolate patient Licheri-2'87)  
 N;Alternate names: HBC antigen  
 N;Contains: core antigen  
 C;Species: hepatitis B virus, HBV  
 A;Variety: isolate patient Licheri-2'87  
 C;Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
 C;Accession: S53270  
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A;Reference number: S53112  
 A;Accession: S53270  
 A;Molecule type: DNA  
 A;Residues: 1-183 <LAI>  
 A;Cross-references: EMBL:X85314; NID:g736201; PIDN:CAA59662.1; PID:g736204  
 A;Experimental source: isolate patient Licheri-2'87  
 A;Note: due to a stop codon between the alternative initiators the e antigen precursor  
 C;Genetics:  
 A;Gene: C  
 C;Superfamily: hepatitis B virus core antigen  
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 0.00066;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 |||||  
 DB 128 TPPAYRPPNAPIL 140

RESULT 9  
 S53129  
 core antigen - hepatitis B virus  
 N;Alternate names: HBC antigen  
 N;Contains: core antigen  
 C;Species: hepatitis B virus, HBV  
 C;Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
 C;Accession: S53129  
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A;Reference number: S53112  
 A;Accession: S53129  
 A;Molecule type: DNA  
 A;Residues: 1-183 <LAI>  
 A;Cross-references: EMBL:X85254; NID:g736003; PIDN:CAA59512.1; PID:g736006

C;Genetics:  
 A;Gene: C  
 C;Superfamily: hepatitis B virus core antigen  
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 0.00066;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 |||||  
 DB 128 TPPAYRPPNAPIL 140

RESULT 10  
 S53140  
 core antigen - hepatitis B virus (isolate patient Frailis'92)  
 N;Alternate names: HBC antigen  
 N;Contains: core antigen  
 C;Species: hepatitis B virus, HBV  
 A;Variety: isolate patient Frailis'92  
 C;Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
 C;Accession: S53140  
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A;Reference number: S53112  
 A;Accession: S53140  
 A;Molecule type: DNA  
 A;Residues: 1-183 <LAI>  
 A;Cross-references: EMBL:X85265; NID:g736017; PIDN:CAA59544.1; PID:g736020  
 A;Experimental source: isolate patient Frailis'92  
 A;Note: due to a stop codon between the alternative initiators the e antigen precursor  
 C;Genetics:  
 A;Gene: C  
 C;Superfamily: hepatitis B virus core antigen  
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 0.00066;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 |||||  
 DB 128 TPPAYRPPNAPIL 140

RESULT 11  
 S53152  
 core antigen - hepatitis B virus (isolate patient Tufariello'89)  
 N;Alternate names: HBC antigen  
 N;Contains: core antigen  
 C;Species: hepatitis B virus, HBV  
 A;Variety: isolate patient Tufariello'89  
 C;Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
 C;Accession: S53152  
 R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A;Reference number: S53112  
 A;Accession: S53152  
 A;Molecule type: DNA  
 A;Residues: 1-183 <LAI>  
 A;Cross-references: EMBL:X85269; NID:g736033; PIDN:CAA59556.1; PID:g736036  
 A;Experimental source: isolate patient Tufariello'89  
 A;Note: due to a stop codon between the alternative initiators the e antigen precursor  
 C;Genetics:  
 A;Gene: C  
 C;Superfamily: hepatitis B virus core antigen  
 C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 0.00066;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 Db 128 TPPAYRPPNAPIL 140

## RESULT 12

core antigen - hepatitis B virus (isolate patient Tedde'89)

N:Alternate names: HBC antigen

N:Contains: core antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Tedde'89

C>Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999

C:Accession: S53166

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53166

A:Molecule type: DNA

A:Residues: 1-183 <LAI>

A:Cross-references: EMBL:X85274; NID:g736053; PIDN:CAA59568.1; PID:g736056

A:Experimental source: isolate patient Tedde'89

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 Db 128 TPPAYRPPNAPIL 140

## RESULT 13

core antigen - hepatitis B virus (isolate patient Muresu'89)

N:Alternate names: HBC antigen

N:Contains: core antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Muresu'89

C>Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999

C:Accession: S53169

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53169

A:Molecule type: DNA

A:Residues: 1-183 <LAI>

A:Cross-references: EMBL:X85275; NID:g736057; PIDN:CAA59571.1; PID:g736060

A:Experimental source: isolate patient Muresu'89

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 Db 128 TPPAYRPPNAPIL 140

## RESULT 14

S53172

core antigen - hepatitis B virus (isolate patient Urtis'89)

N:Alternate names: HBC antigen

N:Contains: core antigen  
 C:Species: hepatitis B virus, HBV  
 A:Variety: isolate patient Urtis'89  
 C>Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
 C:Accession: S53172  
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A:Reference number: S53112  
 A:Accession: S53172  
 A:Molecule type: DNA  
 A:Residues: 1-183 <LAI>

A:Cross-references: EMBL:X85276; NID:g736061; PIDN:CAA59574.1; PID:g736064

A:Experimental source: isolate patient Urtis'89

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 128 TPPAYRPPNAPIL 140

## RESULT 15

core antigen - hepatitis B virus (isolate patient Boi'90)

N:Alternate names: HBC antigen

N:Contains: core antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Boi'90

C>Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999

C:Accession: S53175

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53175

A:Molecule type: DNA

A:Residues: 1-183 <LAI>

A:Cross-references: EMBL:X85277; NID:g736065; PIDN:CAA59577.1; PID:g736068

A:Experimental source: isolate patient Boi'90

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 128 TPPAYRPPNAPIL 140

Search completed: August 9, 2004, 13:29:18

Job time: 16 secs





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FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21095 MW; ED2DA1DB07FB596D CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 2
CORR HPBVJ
ID CORR HPBVJ STANDARD; PRT; 183 AA.
AC P1735L;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adw / strain Japan/PJ2333).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10413;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.,
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).

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EMBL; D00329; -; NOT ANNOTATED_CDS.
PIR; A28925; NKVLJ1.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5F5AF5E160 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 3
CORR HPBVL
ID CORR HPBVL STANDARD; PRT; 183 AA.
AC P1290L;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86258473; PubMed=2638576;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.,
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).

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EMBL; D00329; -; NOT ANNOTATED_CDS.
PIR; A28925; NKVLJ1.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21224 MW; 9FDD6B5F5AF5E160 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 4
CORR HPBVO
ID CORR HPBVO STANDARD; PRT; 183 AA.
AC P17392;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Core antigen.
OS Hepatitis B virus (subtype adw / strain Okinawa/PODW282).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.,
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).

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EMBL; D00330; -; NOT ANNOTATED_CDS.
PIR; B28925; NKVLJ2.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
Core protein; Repeat.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21081 MW; 66BDB2633122930C CRC64;

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OX NCBI\_TaxID=10419;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81012115; PubMed=399329;  
RA Pasek M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,  
RA Leadbetter G., Murray K.,  
RT "Hepatitis B virus genes and their expression in E. coli.",  
RL Nature 282:575-579 (1979).  
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CC -----  
DR EMBL; J02202; AAA45486.1; -  
DR EMBL; A08967; CAA00816.1; -  
DR PIR; B93217; NKVLA2.  
DR InterPro; IPR002006; Hepatitis\_core.  
DR Pfam; PF00906; Hepatitis\_core; 1.  
KW Core protein; Repeat.  
FT REPEAT 162 169  
FT REPEAT 170 177  
SQ SEQUENCE 183 AA; 21042 MW; 545ED0B55527F26C CRC64;  
  
Query Match 100.0%; Score 74; DB 1; Length 183;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TPPAYRPPNAPIL 13  
Db 128 TPPAYRPPNAPIL 140  
  
RESULT 7  
COR\_A HPBV2 STANDARD; PRT; 185 AA.  
AC P03149; 1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Core antigen.  
GN C.  
OS Hepatitis B virus (subtype adw2).  
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10408;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.,  
RL (in) Field B.N., Jaenisch R., Fox C.F. (eds.);  
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).  
DR InterPro; IPR002006; Hepatitis\_core.  
DR Pfam; PF00906; Hepatitis\_core; 1.  
KW Core protein; Repeat.  
FT REPEAT 164 171  
FT REPEAT 172 179  
SQ SEQUENCE 185 AA; 21304 MW; 31F4DC338B507E19 CRC64;  
  
Query Match 100.0%; Score 74; DB 1; Length 185;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TPPAYRPPNAPIL 13  
Db 128 TPPAYRPPNAPIL 140  
  
RESULT 8  
COR\_A HPBVW STANDARD; PRT; 185 AA.  
ID COR\_A HPBVW  
AC P03149;

QY 1 TPPAYRPPNAPIL 13  
Db 128 TPPAYRPPNAPIL 140  
  
RESULT 5  
COR\_A HPBVY STANDARD; PRT; 183 AA.  
AC P03146;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Core antigen.  
GN C.  
OS Hepatitis B virus (subtype ayw).  
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10418;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81012091; PubMed=399327;  
RA Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  
RT cloned in E. coli.",  
RL Nature 281:646-650 (1979).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Latvia;  
RX MEDLINE=85204397; PubMed=3996597;  
RA Bichko V., Pushko P., Dreilina D., Pumpen P., Gren E.;  
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure  
RT analysis.",  
RL FEBS Lett. 185:208-212 (1985).  
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CC -----  
DR EMBL; V01460; CAA24706.1; ALT\_INIT.  
DR EMBL; X02496; -; NOT ANNOTATED CDS.  
DR InterPro; IPR002006; Hepatitis\_core.  
DR Pfam; PF00906; Hepatitis\_core; 1.  
KW Core protein; Repeat.  
FT REPEAT 162 169  
FT REPEAT 170 177  
FT VARIANT 33 33  
FT VARIANT 80 80  
SQ SEQUENCE 183 AA; 21116 MW; E0D9D9763F24E958 CRC64;  
  
Query Match 100.0%; Score 74; DB 1; Length 183;  
Best Local Similarity 100.0%; Pred. No. 0.00053;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TPPAYRPPNAPIL 13  
Db 128 TPPAYRPPNAPIL 140  
  
RESULT 6  
COR\_A HPBVZ STANDARD; PRT; 183 AA.  
AC P03147;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-OCT-1989 (Rel. 12, Last annotation update)  
DE Core antigen.  
GN C.  
OS Hepatitis B virus (subtype adyw).  
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.

```

DB 21-JUL-1986 (Rel. 01, Created)
DB 21-JUL-1986 (Rel. 01, Last sequence update)
DB 01-OCT-1989 (Rel. 12, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw).
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=106821;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RL DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757(1983).
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CC -----
CC EMBL; V00866; ; NOT ANNOTATED CDS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21394 MW; B86A90D541BA70F9 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 9
CORA HPBVF STANDARD; PRT; 195 AA.
ID CORA HPBVF STANDARD; PRT; 195 AA.
AC P29178;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw2 variant sf).
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169850; PubMed=2307406;
RA Bhat R.A., Ulrich P.P., Vyas G.N.;
RT "Molecular characterization of a new variant of hepatitis B virus in
RT a persistently infected homosexual man.";
RL Hepatology 11:271-276(1990).
DR PIR; A37182; NKVLH3.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 174 181
FT REPEAT 182 189
SQ SEQUENCE 195 AA; 22461 MW; E2B166F879CB7CRC64;

Query Match 100.0%; Score 74; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

DB 140 TPPAYRPPNAPIL 152

RESULT 10
CORA HPBVA STANDARD; PRT; 211 AA.
ID CORA HPBVA STANDARD; PRT; 211 AA.
AC P24023;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain alpha1).
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90266476; PubMed=2345966;
RA Tong S., Li J., Witvitski L., Trepo C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
RT associated with viral variants containing an inactive pre-C region.";
RL Virology 176:596-603(1990).
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CC -----
CC EMBL; X32138; ; NOT ANNOTATED CDS.
DR PIR; A34773; NKVLAL.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 183 190
FT REPEAT 198 206
SQ SEQUENCE 211 AA; 24208 MW; B774AC72B65C75AB CRC64;

Query Match 100.0%; Score 74; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 156 TPPAYRPPNAPIL 168

RESULT 11
CORA HPBVT STANDARD; PRT; 212 AA.
ID CORA HPBVT STANDARD; PRT; 212 AA.
AC Q05495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=45410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HSV surface antigen subtype adw4.";
RL J. Gen. Virol. 74:1627-1632(1993).
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RT shows conservation of the genome." ;
RL Virology 162:12-20(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=woodchuck hepatitis virus 8 (infectious clone);
RX MEDLINE=89184524; PubMed=2928306;
RA Gitones R., Cote P.J., Hornbuckle W.B., Tennant B.C., Gerin J.L.,
RA Purcell R.H., Miller R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
RT hepatitis virus that is infectious in the natural host." ;
RL Proc. Natl. Acad. Sci. U.S.A. 86:1846-1849(1989).
RN [3]
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CC -----
DR EMBL; J02442; AAA46761.1; -
DR EMBL; M18752; AAA46769.1; -
DR EMBL; M19183; AAA46765.1; -
DR EMBL; J04514; AAA46772.1; -
DR PIR; C32397; NKVLC.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MW; 1F4454D0A7B7CE42 CRC64;
Query Match 82.4%; Score 61; DB 1; Length 188;
Best Local Similarity 84.6%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TPPAYRPPNPAPIL 13
DB 128 TPAPYRPPNPAPIL 140
RESULT 15
COR_A_HPBGS STANDARD; PRT; 217 AA.
AC P03153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE Core antigen.
GN C.
OS Ground squirrel hepatitis virus (GSV).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10406;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84267998; PubMed=6086950;
RA Seeger C., Ganem D., Varmus H.E.;
RT "Nucleotide sequence of an infectious molecularly cloned genome of
RT ground squirrel hepatitis virus." ;
RL J. Virol. 51:367-375(1984).
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CC -----
DR EMBL; K02715; AAA46755.1; -
DR PIR; A03715; NKVLS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
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KW Core protein; Repeat.
FT REPEAT 196 203
FT REPEAT 204 211
SQ SEQUENCE 217 AA; 25189 MW; DF489467355EC11A CRC64;
Query Match 82.4%; Score 61; DB 1; Length 217;
Best Local Similarity 84.6%; Pred. No. 0.046;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TPPAYRPPNPAPIL 13
DB 157 TPAPYRPPNPAPIL 169
Search completed: August 9, 2004, 13:28:04
Job time : 13 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 9, 2004, 13:27:00 ; Search time 35 Seconds

(without alignments)  
117.192 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TTPAYRPPNPAPIL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp archaea:\*
- 2: sp bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	74	100.0	96	12	Q9YQ42 hepatitis b
2	74	100.0	96	12	Q9YJM3 hepatitis b
3	74	100.0	113	12	Q80J61 hepatitis b
4	74	100.0	130	12	Q8QP24 hepatitis b
5	74	100.0	130	12	Q8QPI1 hepatitis b
6	74	100.0	130	12	Q8JSV0 hepatitis b
7	74	100.0	130	12	Q8QP22 hepatitis b
8	74	100.0	130	12	Q8JSW1 hepatitis b
9	74	100.0	130	12	Q8JSV2 hepatitis b
10	74	100.0	130	12	Q8JSV9 hepatitis b
11	74	100.0	130	12	Q8QPI9 hepatitis b
12	74	100.0	130	12	Q8JSV1 hepatitis b
13	74	100.0	130	12	Q8JSW5 hepatitis b
14	74	100.0	130	12	Q8JSW9 hepatitis b
15	74	100.0	130	12	Q8QP32 hepatitis b
16	74	100.0	130	12	Q8JSV3 hepatitis b

17	74	100.0	130	12	Q8QP23	hepatitis b
18	74	100.0	130	12	Q8QPI1	hepatitis b
19	74	100.0	130	12	Q8QP25	hepatitis b
20	74	100.0	130	12	Q8QPI6	hepatitis b
21	74	100.0	130	12	Q8QPI1	hepatitis b
22	74	100.0	130	12	Q8QP27	hepatitis b
23	74	100.0	130	12	Q8JSW3	hepatitis b
24	74	100.0	130	12	Q8JSX0	hepatitis b
25	74	100.0	130	12	Q8QP29	hepatitis b
26	74	100.0	130	12	Q8QP34	hepatitis b
27	74	100.0	130	12	Q8JSW7	hepatitis b
28	74	100.0	130	12	Q8JSX5	hepatitis b
29	74	100.0	130	12	Q8JSV5	hepatitis b
30	74	100.0	130	12	Q8JSW8	hepatitis b
31	74	100.0	130	12	Q8QP30	hepatitis b
32	74	100.0	130	12	Q8QPI17	hepatitis b
33	74	100.0	130	12	Q8JSW2	hepatitis b
34	74	100.0	130	12	Q8JSX1	hepatitis b
35	74	100.0	130	12	Q8JSV6	hepatitis b
36	74	100.0	130	12	Q8QPI3	hepatitis b
37	74	100.0	130	12	Q8JSW4	hepatitis b
38	74	100.0	130	12	Q8QPI8	hepatitis b
39	74	100.0	130	12	Q8QP26	hepatitis b
40	74	100.0	130	12	Q8JSV4	hepatitis b
41	74	100.0	130	12	Q8JSW6	hepatitis b
42	74	100.0	130	12	Q8QP28	hepatitis b
43	74	100.0	130	12	Q8QPI5	hepatitis b
44	74	100.0	130	12	Q8JSW0	hepatitis b
45	74	100.0	130	12	Q8JSX3	hepatitis b

#### ALIGNMENTS

RESULT 1

ID Q9YQ42 PRELIMINARY; PRT; 96 AA.  
AC Q9YQ42;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Core antigen (Fragment).  
GN C.  
OS Hepatitis B virus.  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10407;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=genotype D;  
RX MEDLINE=20381124; PubMed=10921962;  
RA Petrosillo N., Ippolito G., Solfrosi L, Varaldo P.E., Clementi M.,  
RA Manzin A.;  
RT "Molecular epidemiology of an outbreak of fulminant Hepatitis B.";  
RL J. Clin. Microbiol. 38:2975-2981(2000).  
DR EMBL; AJ010001; CAA08950.1; -;  
DR InterPro; IPR002006; Hepatitis core.  
DR Pfam; PF00906; Hepatitis\_core; 1.  
FT NON\_TER 1  
SQ SEQUENCE 96 AA; 11428 MW; D46972F6440979BE CRC64;

Query Match 100.0%; Score 74; DB 12; Length 96;  
Best Local Similarity 100.0%; Pred. No. 0.00029;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPAYRPPNPAPIL 13  
Db 41 TTPAYRPPNPAPIL 53

RESULT 2

Q9YJM3 PRELIMINARY; PRT; 96 AA.  
ID Q9YJM3  
AC Q9YJM3;

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01-MAY-1999 (TREMBlrel. 10, Created)
01-MAY-1999 (TREMBlrel. 10, Last sequence update)
01-OCT-2002 (TREMBlrel. 22, Last annotation update)
01-OCT-2002 (TREMBlrel. 22, Last annotation update)
Core antigen (Fragment).
GN C.
Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RC STRAIN=GENOTYPE D;
RP SEQUENCE FROM N.A.
RA Manzin A.;
RT "An outbreak of fulminant hepatitis B in a haematologic unit (Pesaro, Italy), part 2."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010007; CAA08962.1; -
DR EMBL; AJ009994; CAA08936.1; -
DR EMBL; AJ009995; CAA08938.1; -
DR EMBL; AJ009996; CAA08940.1; -
DR EMBL; AJ009997; CAA08942.1; -
DR EMBL; AJ009998; CAA08944.1; -
DR EMBL; AJ009999; CAA08946.1; -
DR EMBL; AJ010000; CAA08948.1; -
DR EMBL; AJ010002; CAA08952.1; -
DR EMBL; AJ010003; CAA08954.1; -
DR EMBL; AJ010004; CAA08956.1; -
DR EMBL; AJ010005; CAA08958.1; -
DR EMBL; AJ010006; CAA08960.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER
SQ SEQUENCE 96 AA; 11443 MW; FBA862E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 12; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 41 TPPAYRPPNAPIL 53

RESULT 3
Q8QJ61 PRELIMINARY; PRT; 113 AA.
AC Q8QJ61;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Core protein.
OS Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RC STRAIN=7-2;
RP SEQUENCE FROM N.A.
RA Luo K., Liu Z., He H., Liang W., Peng J., Dai W., Hou J.;
RT "The putative recombination of hepatitis B virus genotype B with pre-C/C of genotype C."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY217370; AAO63544.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
SQ SEQUENCE 113 AA; 13068 MW; 3A0E460F2038C680 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 58 TPPAYRPPNAPIL 70

RESULT 4
Q8QP24 PRELIMINARY; PRT; 130 AA.
AC Q8QP24;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Core protein (fragment).
GN C.
Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RC STRAIN=45B;
RA Dumpis U., Jansons J., Solominskaya I., Michailova M., Pumpens P.;
RT "Containment of the outbreak of Hepatitis B and C infection in a Latvian pediatric oncology ward."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079230; AAM11934.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER
SQ SEQUENCE 130 AA; 15151 MW; E32DD1DB4B4D51DC CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 75 TPPAYRPPNAPIL 87

RESULT 5
Q8QP11 PRELIMINARY; PRT; 130 AA.
AC Q8QP11;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Core protein (fragment).
GN C.
Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RC STRAIN=9latvia;
RA Dumpis U., Jansons J., Solominskaya I., Michailova M., Pumpens P.;
RT "Containment of the outbreak of Hepatitis B and C infection in a Latvian pediatric oncology ward."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079243; AAM11947.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER
SQ SEQUENCE 130 AA; 15065 MW; 45D8AB909ECD9BAE CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 75 TPPAYRPPNAPIL 87

RESULT 6
Q8JSV0 PRELIMINARY; PRT; 130 AA.
AC Q8JSV0;
ID Q8JSV0

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GN 01-OCT-2002 (TrEMBLrel. 22, Created)
OS 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
OC 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Core protein (Fragment).
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR4.2/X;
RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
RT "Genotype mixtures of hepatitis B virus in patients treated with
interferon.";
RL J. Infect. Dis. 0:0-0(2002).
DR EMBL; AF474403; AAM70081.1; --
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 14606 MW; C9D9EDCEFE150158 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 111 TPPAYRPPNAPIL 123

RESULT 7
Q8QP22
ID Q8QP22 PRELIMINARY; PRT; 130 AA.
AC Q8QP22;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Core protein (Fragment).
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=24B;
RA Dumpis U., Jansons J., Solominskaya I., Michailova M., Pumpens P.;
RT "Containment of the outbreak of Hepatitis B and C infection in a
Latvian pediatric oncology ward.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079232; AAM11936.1; --
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15068 MW; E56F3FDCD7D351DC CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 75 TPPAYRPPNAPIL 87

RESULT 8
Q8JSW1
ID Q8JSW1 PRELIMINARY; PRT; 130 AA.
AC Q8JSW1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Core protein (Fragment).

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GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LR3.1/A;
RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
RT "Genotype mixtures of hepatitis B virus in patients treated with
interferon.";
RL J. Infect. Dis. 0:0-0(2002).
DR EMBL; AF474392; AAM70070.1; --
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 14744 MW; 4792F0C7FIC0DA8A CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 111 TPPAYRPPNAPIL 123

RESULT 9
Q8JSV2
ID Q8JSV2 PRELIMINARY; PRT; 130 AA.
AC Q8JSV2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Core protein (Fragment).
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SR6.2/X;
RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
RT "Genotype mixtures of hepatitis B virus in patients treated with
interferon.";
RL J. Infect. Dis. 0:0-0(2002).
DR EMBL; AF474401; AAM70079.1; --
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 14708 MW; 0B393223D37604D1 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 111 TPPAYRPPNAPIL 123

RESULT 10
Q8JSV9
ID Q8JSV9 PRELIMINARY; PRT; 130 AA.
AC Q8JSV9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Core protein (Fragment).
GN Hepatitis B virus.
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC

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OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LR4.1/A;
RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
RT "Genotype mixtures of hepatitis B virus in patients treated with
interferon.";
RL J. Infect. Dis. 0:0-0(2002).
DR EMBL; AF474402; AAM70080.1;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 14708 MW; 0B393223D37604D1 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 111 TPPAYRPPNAPIL 123

RESULT 11
Q8QPI9 PRELIMINARY; PRT; 130 AA.
AC Q8QPI9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Core protein (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Dumps U., Jansons J., Solominskaya I., Michailova M., Pumpens P.;
RT "Containment of the outbreak of Hepatitis B and C infection in a
Latvian pediatric oncology ward.";
RL Submitted (FEF-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079235; AAM11939.1;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 130 AA; 15136 MW; 04BA4FDCD7DD51D8 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 75 TPPAYRPPNAPIL 87

RESULT 12
Q8JSV1 PRELIMINARY; PRT; 130 AA.
AC Q8JSV1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Core protein (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SR6.2/X2;
RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
RT "Genotype mixtures of hepatitis B virus in patients treated with
interferon.";
RL J. Infect. Dis. 0:0-0(2002).
DR EMBL; AF474402; AAM70080.1;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 14708 MW; 0B393223D37604D1 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 111 TPPAYRPPNAPIL 123

RESULT 13
Q8JSW5 PRELIMINARY; PRT; 130 AA.
AC Q8JSW5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Core protein (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
RT "Genotype mixtures of hepatitis B virus in patients treated with
interferon.";
RL J. Infect. Dis. 0:0-0(2002).
DR EMBL; AF474388; AAM70066.1;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 14628 MW; 48EF8BE4C0D21408 CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 111 TPPAYRPPNAPIL 123

RESULT 14
Q8JSW9 PRELIMINARY; PRT; 130 AA.
AC Q8JSW9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Core protein (Fragment).
GN C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rel4.1/AL;
RA Hannoun C., Krogsgaard K., Horal P., Lindh M.;
RT "Genotype mixtures of hepatitis B virus in patients treated with
interferon.";
RL J. Infect. Dis. 0:0-0(2002).

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DR ENBL; AF474384; AAM70062.1; -.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 14744 MW; 4792F0C7F1C0D8A CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
Db 111 TPPAYRPPNPAPIL 123
|||||
|||||

RESULT 15
Q8QP32 PRELIMINARY; PRT; 130 AA.
AC Q8QP32;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Core protein (Fragment).
DE C.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2T;
RA Dumpis U., Jansons J., Solominskaya I., Michailova M., Pumpens P.;
RT "Containment of the outbreak of Hepatitis B and C infection in a
RT Latvian pediatric oncology ward";
RL Submitted (FEBS-2002) to the ENBL/GenBank/DBJ databases.
RL ENBL; AY079222; AAM11926.1; -.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 1
FT NON_TER 130 AA; 15137 MW; E4B44FDCD7D351DC CRC64;

Query Match 100.0%; Score 74; DB 12; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNPAPIL 13
Db 75 TPPAYRPPNPAPIL 87
|||||
|||||

Search completed: August 9, 2004, 13:28:52
Job time : 36 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2004, 18:26:45 ; Search time 50 Seconds

(without alignments)  
73.462 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TTPAYRPPNAPIL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 383904

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	13	2	AAR33501 T helper
2	74	100.0	13	2	Aar78929 HBC 128-1
3	74	100.0	13	2	Aw39439 Mouse H-2
4	74	100.0	13	2	AAW50117 Pan DR bi
5	74	100.0	13	3	AAY52556 HBV core
6	74	100.0	13	3	AAAG64542 T-helper
7	74	100.0	13	4	AAE02681 Hepatitis
8	74	100.0	13	4	AAE00471 Hepatitis
9	74	100.0	13	4	AAE02626 Immunogen
10	74	100.0	13	4	AAE02626 Immunogen
11	74	100.0	13	4	AAE02626 Immunogen
12	74	100.0	13	5	AAU070851 Hepatitis
13	74	100.0	13	5	ABE76787 HBV pepti
14	74	100.0	13	5	ABG62860 Antigenic
15	74	100.0	13	5	ABP52344 TH epitop
16	74	100.0	13	5	ABP52307 T helper
17	74	100.0	13	5	ABP52350 TH epitop
18	74	100.0	13	5	ABP51503 T helper
19	74	100.0	13	5	ABR44095 HBV core
20	74	100.0	13	6	ABP98778 HBV core
21	74	100.0	13	6	AAO22990 p128-40 I
22	74	100.0	13	6	ABU63009 HBV core
23	74	100.0	13	7	ADC21494 Hepatitis
24	74	100.0	13	7	ADC85105 HBV assoc
25	74	100.0	13	7	ADD35647 Hepatitis

26	69	93.2	12	1	AAP80957 T cell st
27	69	93.2	13	6	ADA51351 Hepatitis
28	65	87.8	11	5	ABJ06979 Hepatitis
29	65	87.8	11	5	ABJ07803 Hepatitis
30	65	87.8	12	6	ADA51350 Hepatitis
31	65	87.8	13	6	ADA51364 Hepatitis
32	64	86.5	12	6	ADA51337 Hepatitis
33	64	86.5	13	6	ADA51338 Hepatitis
34	62	83.8	11	5	ABJ07363 Hepatitis
35	62	83.8	11	5	ABJ06223 Hepatitis
36	61	82.4	11	6	ADA51349 Hepatitis
37	61	82.4	12	6	ADA51363 Hepatitis
38	61	82.4	13	6	ADA51377 Hepatitis
39	60	81.1	11	6	ADA51336 Hepatitis
40	59	79.7	10	2	AAV47999 Immunogen
41	59	79.7	10	5	ABJ07000 Hepatitis
42	59	79.7	10	5	ABJ07724 Hepatitis
43	59	79.7	11	5	ABJ06294 Hepatitis
44	59	79.7	11	5	ABJ08210 Hepatitis
45	59	79.7	11	5	ABJ07371 Hepatitis

ALIGNMENTS

RESULT 1  
AAR33501  
ID AAR33501 standard; peptide; 13 AA.

AC AAR33501;  
XX  
DT 25-MAR-2003 (revised)  
DT 01-JUL-1993 (first entry)  
XX  
DE T helper peptide HBC 128-140.  
XX  
KW Hepatitis B virus; HBV; core antigen; MHC class I; chronic; acute;  
infection; identification; HLA-restricted.  
XX  
OS Synthetic.  
XX  
PN WO9303764-A1.  
XX  
PD 04-MAR-1993.  
XX  
PF 26-AUG-1992; 92WO-US007218.  
XX  
PR 26-AUG-1991; 91US-00749568.  
PR 29-JAN-1992; 92US-00827682.  
PR 27-APR-1992; 92US-00874491.  
XX  
PA (CYTE-) CYTEL CORP.  
XX  
PI Vitello MA, Chesnut RW;  
XX  
DR WPI; 1993-093728/11.  
XX  
PT Cytotoxic T-lymphocyte stimulating peptide(s) - derived from hepatitis B  
XX  
FT virus useful for treating, preventing and diagnosing infection.  
XX  
PS Disclosure; Page 21; 89pp; English.  
XX  
CC This is a T helper epitope peptide, the sequence of which is derived from  
XX  
CC hepatitis B virus (HBV) core antigen amino acids 128-140. It may be used  
XX  
CC in a conjugate with cytotoxic T-lymphocyte stimulating (CTL) peptides to  
XX  
CC enhance an individual's immunity by providing cell-mediated immunity and  
XX  
CC protective antibodies. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 DB 1 TPPAYRPPNAPIL 13

RESULT 2  
 AAR78929  
 ID AAR78929 standard; peptide; 13 AA.  
 XX  
 AC AAR78929;  
 DT 25-MAR-2003 (revised)  
 DT 27-MAR-1996 (first entry)  
 XX  
 DE HBC 128-140 cytotoxic T lymphocyte epitope.  
 XX  
 KW HBC 128-140; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte;  
 KW antigens; treatment; disease prevention; hepatitis B.  
 XX  
 OS Hepatitis B virus.  
 XX  
 FN W09522317-A1.  
 XX  
 PD 24-AUG-1995.  
 XX  
 PF 16-FEB-1995; 95WO-US002121.  
 XX  
 PR 16-FEB-1994; 94US-00197484.  
 XX  
 PA (CYTE-) CYTEL CORP.  
 PI Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;  
 XX  
 DR WPI; 1995-302545/39.  
 XX  
 PT Compn. inducing cytotoxic T lymphocyte response to pref. viral,  
 PT bacterial, parasitic or tumour antigens - useful in the treatment and  
 PT prevention of diseases associated with the antigen e.g. hepatitis B.  
 XX  
 PS Example 4; Page 52; 109pp; English.  
 CC A compen. which induces a cytotoxic T lymphocyte (CTL) response to a  
 CC hepatitis B virus (HBV) antigen (Ag) in a mammal comprises, a HBV CTL Ag  
 CC response inducing peptide (i.e. AAR78929) and a lipid conjugated helper T  
 CC cell inducing peptide. The compn. is useful in the treatment and  
 CC prevention of hepatitis B. (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 DB 1 TPPAYRPPNAPIL 13

RESULT 3  
 AAW39439  
 ID AAW39439 standard; peptide; 13 AA.  
 XX  
 AC AAW39439;  
 DT 11-JUN-1998 (first entry)  
 XX  
 DE Mouse H-2 I-Ab-restricted HBV core antigen-derived T helper epitope.  
 XX  
 KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;  
 KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;  
 KW disease; anti-tumour; anti-viral.  
 XX

OS Synthetic.  
 OS Mus sp.  
 XX  
 PN W09741440-A1.  
 XX  
 PD 06-NOV-1997.  
 XX  
 PF 28-APR-1997; 97WO-NL000229.  
 XX  
 PR 26-APR-1996; 96EP-00201145.  
 PR 23-DEC-1996; 96EP-00203670.  
 XX  
 PA (UYLE-) RIJCSUNIV LEIDEN.  
 PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.  
 XX  
 PI Van Der Burg SH, Kast WM, Tees REM, Offringa R, Melief CJM;  
 XX  
 DR WPI; 1997-549891/50.  
 XX  
 PT Method of selecting T cell peptide epitope(s) - by measuring the  
 PT stability of HLA class I-peptide complexes on intact B cells.  
 XX  
 PS Example 2; Page 21; 109pp; English.  
 XX  
 CC Peptides AAW39430-W39734 are used in a novel method for the selection of  
 CC immunogenic T-cell peptide epitopes present in polypeptide antigens.  
 CC Peptide AAW39439 is a mouse H-2 I-Ab restricted HBV core antigen-derived  
 CC T helper epitope which is injected into HLA-A\*0201Kb transgenic mice. The  
 CC method involves the identification of peptide sequences capable of  
 CC binding to an HLA (human leukocyte antigen) class I molecule and  
 CC measuring the binding of this epitope peptide to the HLA class I peptide.  
 CC The stability of binding of the peptide and MHC (major histocompatibility  
 CC complex) class I molecule is measured on intact human B cells carrying  
 CC the MHC molecule at their cell surfaces. The method can be used to select  
 CC peptide epitopes for generating vaccines against a disease associated  
 CC with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are  
 CC especially T-cell peptide epitopes with strong anti-tumour and anti-viral  
 CC immune responses  
 XX  
 SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 DB 1 TPPAYRPPNAPIL 13

RESULT 4  
 AAW50117  
 ID AAW50117 standard; peptide; 13 AA.  
 XX  
 AC AAW50117;  
 DT 30-JUN-1998 (first entry)  
 XX  
 DE Pan DR binding peptide (14).  
 XX  
 KW Pan DR binding peptide; antigen binding site; MHC molecule; DR locus.  
 XX  
 OS Synthetic.  
 XX  
 PN US5736142-A.  
 XX  
 PD 07-APR-1998.  
 XX  
 PF 14-SEP-1994; 94US-00305871.  
 XX  
 PR 14-SEP-1993; 93US-00121101.  
 XX  
 PA (CYTE-) CYTEL CORP.

XX Sidney J, Sette A, Alexander JL, Gaeta F, Grey HM;  
 XX WPI; 1998-239154/21.  
 XX  
 XX Peptides that bind to MHC molecules of all DR alleles - inhibiting or  
 XX inducing MHC Class II mediated activation of T cells.  
 XX  
 XX Example 5; Col 35-36; 29pp; English.  
 XX  
 XX The present sequence, a pan DR binding peptide, is capable of binding  
 XX antigen binding sites on MHC molecules, which are encoded by most of the  
 XX alleles of a DR locus. The peptide can be used to inhibit or induce MHC  
 XX class II mediated activation of T-cells or helper T-cells, which  
 XX themselves mediate a CTL response. The peptide can be used in mammals,  
 XX especially humans, to inhibit T-cell-mediated events involved in  
 XX allograft rejection, allergic responses and autoimmunity and as a vaccine  
 XX adjuvant for enhancing an immune response against an administered  
 XX immunogen. The peptide can be used with other immunogens to treat, e.g.  
 XX prostate cancer, hepatitis B, hepatitis C, AIDS, renal and cervical  
 XX carcinoma, lymphoma, CMV and condyloma acuminatum  
 XX  
 XX Sequence 13 AA;  
 XX  
 XX Query Match 100.0%; Score 74; DB 2; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 0.0011;  
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 TPPAYRPPNAPIL 13  
 XX Db |||||  
 XX 1 TPPAYRPPNAPIL 13  
 XX  
 XX RESULT 5  
 XX AAY52556  
 XX ID AAY52556 standard; peptide; 13 AA.  
 XX AC  
 XX AAY52556;  
 XX  
 XX 06-AUG-2003 (revised)  
 XX 28-FEB-2000 (first entry)  
 XX  
 XX HBV core antigen MHC class II epitope, encoded by 180T fusion gene.  
 XX  
 XX Chimeric; pan DR epitope; expression vector; promoter;  
 XX major histocompatibility complex; MHC; targeting; peptide; epitope;  
 XX antigen; presentation; class I; cytosolic pathway; endoplasmic reticulum;  
 XX class II, extracellular antigen; endocytic pathway; helper T lymphocyte;  
 XX HLA; universal epitope; cytotoxic T lymphocyte; CTL; immune response;  
 XX immunogenicity; assay; vaccine; immunity; infection; pathogen; virus;  
 XX HIV; HBV; HCV; hepatitis B; hepatitis C; bacterium; protozoan;  
 XX tumour cell; autoimmune disease; activation; antiviral; antimalarial;  
 XX immunoprotective; core antigen.  
 XX  
 XX Synthetic.  
 XX Hepatitis B virus.  
 XX  
 XX WO9958658-A2.  
 XX  
 XX 18-NOV-1999.  
 XX  
 XX 13-MAY-1999; 99WO-US010646.  
 XX  
 XX 13-MAY-1998; 98US-00078904.  
 XX 15-MAY-1998; 98US-0085751P.  
 XX  
 XX (EPIM-) EPIMUNE INC.  
 XX  
 XX Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;  
 XX Chesnut RW;  
 XX WPI; 2000-039103/03.  
 XX

PT	Expression vectors encoding major histocompatibility targeting sequence,
FT	used as, e.g. tumor vaccines.
XX	
XX	Example 1; Page 36; 130pp; English.
XX	
CC	This sequence represents a hepatitis B virus (HBV) core antigen MHC class
CC	II epitope, encoded by the I80T fusion gene (AAZ38617), used in an
CC	exemplification of the present invention. The invention relates to a
CC	novel expression vector comprising a promoter operably linked to a fusion
CC	gene encoding a major histocompatibility complex (MHC) targeting
CC	sequence, and two or more heterologous peptide epitopes. The MHC
CC	targeting sequence may be a class I targeting sequence, which directs
CC	an MHC class I epitope to a cytosolic pathway or to the endoplasmic
CC	reticulum, or an MHC class II targeting sequence, which directs
CC	extracellular antigens to enter the endocytic pathway to be processed
CC	into antigen peptides for presentation on MHC class II molecules. The
CC	heterologous epitopes may comprise either helper T lymphocyte (HTL)
CC	epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL
CC	epitope such as a pan DR epitope (PADRE). The vectors are useful for
CC	stimulating an immune response in vivo, as well as for use in assaying
CC	the human immunogenicity of a human T cell peptide epitope in vivo in a
CC	non-human mammal. They provide a nucleic acid vaccine for enhancing
CC	immunity against infectious pathogens, such as viruses (e.g., HIV,
CC	hepatitis B (HBV) and hepatitis C (HCV)), bacteria, protozoa (e.g.,
CC	Plasmodium falciparum, the cause of malaria) and also tumour cells and
CC	autoimmune diseases. Universal MHC class II epitopes are advantageously
CC	combined with other MHC class I and class II epitopes to increase the
CC	number of cells that are activated in response to a given antigen and
CC	provide a broader population coverage of MHC-reactive alleles. (Updated
CC	on 06-AUG-2003 to correct OS field.)
XX	
SQ	Sequence 13 AA;
	Query Match 100.0%; Score 74; DB 3; Length 13;
	Best Local Similarity 100.0%; Pred. No. 0.0011;
	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 TPPAYRPPNPAPIL 13 
Dd	1 TPPAYRPPNPAPIL 13 
RESULT 6	
AAG64542	
ID	AAG64542 standard; peptide; 13 AA.
AC	AAG64542;
XX	
DT	22-OCT-2001 (first entry)
XX	
DE	T-helper epitope peptide.
XX	
KW	Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
KW	human immunodeficiency virus; vaccine; T-helper.
OS	Synthetic.
XX	
FN	WO200155177-A2.
XX	
PD	02-AUG-2001.
XX	
PF	29-JAN-2001; 2001WO-DK000059.
XX	
PR	28-JAN-2000; 2000EP-00610017.
PR	31-JAN-2000; 2000US-0179333P.
XX	
PA	(STAT-) STATENS SERUM INST.
XX	
PI	Fomsgaard A, Brunak S, Buus S, Corbet S, Laemoller SL, Hansen J;
XX	
DR	WPI; 2001-476184/51.
XX	
PT	The generation of cytotoxic T cell lymphocytes epitopes for use in anti-

PT HIV vaccines.

PS Example 7; Page 42; 383pp; English.

XX The invention relates to identification of cytotoxic T cell lymphocyte

CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL

CC are a major protective mechanism against viral diseases. Antibodies may

CC neutralise extracellular human immunodeficiency virus (HIV) and limit or

CC prevent infection of cells in the host, but CTL will limit viral

CC production by killing the cell. The CTL epitopes are useful in medicine,

CC in the manufacture of vaccines or diagnostic agents. The present sequence

CC is that of a T-helper epitope peptide useful to the invention

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. NO. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 1 TPPAYRPPNAPIL 13

|||||

RESULT 7

AAE02681

ID AAE02681 standard; peptide; 13 AA.

AC AAE02681;

XX

XX 06-AUG-2001 (first entry)

DT Hepatitis B virus HBVc helper peptide.

DE

XX Cytostatic; antibacterial; antifungal; gene therapy; vaccine; antiviral;

XX tumour; epitope; glycoprotein; Hepatitis B virus; HBV; immune response;

KW CTL; cytotoxic T lymphocyte; HLA; human leucocyte antigen.

KW

XX Hepatitis B virus.

OS

XX WO200127291-A1.

PN

XX 19-APR-2001.

PD

XX 29-SEP-2000; 2000WO-EP009902.

PF

XX 12-OCT-1999; 99US-0158356P.

PR

XX (INSP ) INST PASTEUR.

PA

XX Firat H, Lemonnier F, Langlade-Demoyen P;

PI

XX WPI; 2001-282038/29.

DR

XX New polynucleotide comprising at least one viral, fungal, bacterial, or

PT tumor epitope of an antigen, capable of inducing a cellular response.

PS

XX Example 1; Page 23; 70pp; English.

XX The invention relates to polynucleotide containing at least a part of the

CC coding sequence of the middle glycoprotein of hepatitis B virus (HBV) in

CC which is inserted a DNA sequence coding for an epitope comprising at

CC least one viral, fungal, bacterial, or tumour epitope of an antigen,

CC capable of inducing a cellular response. Nucleic acids and compositions

CC of the invention are useful for inducing in vivo a CTL (cytotoxic T

CC lymphocyte) response against several epitopes of one or more, bacterial,

CC viral, fungal, or tumour antigens. A composition of the invention

CC produces an immune response against HIV antigen and are used in the

CC production of vaccines. The polynucleotides of the invention are also

CC used in gene therapy. The present sequence is hepatitis B virus helper

CC peptide. This peptide is co-injected with human epitopes in order to

CC elicit HLA (human leucocyte antigen) -A2.1-restricted CTL response in

CC mice

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. NO. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 1 TPPAYRPPNAPIL 13

|||||

RESULT 8

AAE00471

ID AAE00471 standard; peptide; 13 AA.

XX

AC AAE00471;

XX

XX 19-JUN-2001 (first entry)

DT Hepatitis B virus core (HBVc) tumour epitope peptide.

DE

XX Tumour epitope; cytostatic; immunostimulant; gene therapy;

XX middle glycoprotein; Hepatitis B virus core; cytotoxic response;

KW immune response; cytotoxic T lymphocyte; CTL; HBVc; HLA;

KW human leucocyte antigen.

XX

OS Hepatitis B virus.

XX

XX WO200123577-A2.

PN

XX 05-APR-2001.

PD

XX 29-SEP-2000; 2000WO-EP009900.

PF

XX 30-SEP-1999; 99US-0156945P.

PR

XX (INSP ) INST PASTEUR.

PA

XX Firat H, Lemonnier F, Langlade-Demoyen P, Michel M, Suhrbier AA;

PI

XX WPI; 2001-266164/27.

DR

XX Novel polynucleotide having DNA sequence encoding tumor antigen epitope

PT inserted in part of coding sequence of middle glycoprotein of hepatitis B

PT virus, used to induce immune response against tumor-specific antigen.

XX

PS Example 1; Page 13; 36pp; English.

XX The present invention relates to an isolated or purified polynucleotide

CC containing a DNA sequence coding for at least one tumour epitope of a

CC tumour antigen inserted into part of the coding sequence of the middle

CC glycoprotein of the Hepatitis B virus (HBV). The polynucleotide is useful

CC for optionally evaluating cytotoxic responses in the individual's

CC lymphocyte population. It induces an immune response against at least one

CC tumour specific antigen or tissue specific antigen. The vector comprising

CC the polynucleotide induces in vivo, cellular and/or humoral immune

CC response. The composition comprising the polynucleotide induces in vivo,

CC cytotoxic T lymphocyte (CTL) against one or more antigens or epitopes

CC present on the hybrid protein. The polynucleotide is also useful in gene

CC therapy. The present sequence is a Hepatitis B virus core (HBVc) tumour

CC epitope peptide. This peptide elicits HLA (human leucocyte antigen) -A2.1

CC - restricted CTL response in mice

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. NO. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13

Db 1 TPPAYRPPNAPIL 13

|||||



RESULT 9  
AAG62426  
ID AAG62426 standard; peptide; 13 AA.  
XX  
AC AAG62426;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Immunogenic peptide HBV core SEQ ID 30.  
XX  
KW Class I epitope; immunogenic; heteroclitic analogue; immune response;  
KW antigen display; viral disease; cancer.  
XX  
OS Synthetic.  
XX  
PN WO200136452-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 20-NOV-2000; 2000WO-US031856.  
XX  
PR 18-NOV-1999; 99US-0166529P.  
XX  
PR 06-OCT-2000; 2000US-0239008P.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Tangri S, Sette A, Ishioka G;  
XX  
XX WPI; 2001-355609/37.  
XX  
XX Enhancing immunogenicity of peptide containing class I epitope, useful  
PT for treating cancer, comprises providing (semi-)conservative amino acid  
PT substitutions at specified positions of these epitopes.  
XX  
PS Disclosure; Fig 1A; 96pp; English.  
XX  
CC This invention relates to a method of enhancing the immunogenicity of a  
CC peptide, where the peptide contains a class I epitope. The invention  
CC includes methods for preparing peptides containing epitopes which have  
CC enhanced ability to effect an immune response (compared to wild-type  
CC epitopes). The peptides are referred to as heteroclitic analogues. The  
CC method is useful for eliciting an immune response by contacting CTLs with  
CC the immunogenically enhanced peptide in vitro in the presence of an  
CC antigen presenting cell, or by administering to a subject a nucleic acid  
CC molecule comprising a nucleotide sequence encoding the peptide. The  
CC peptides are useful as reagents to evaluate an immune response and the  
CC efficacy of the vaccine, and for making antibodies. The heteroclitic  
CC analogues are useful in immunological compositions for the treatment of  
CC viral diseases, cancer, and other conditions which are characterised by  
CC displayed antigens on target cells. The present sequence represents a  
CC class I epitope which may be used in the method of the invention  
XX  
SQ Sequence 13 AA;  
Query Match 100.0%; Score 74; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TPPAYRPPNAPIL 13  
DB 1 TPPAYRPPNAPIL 13  
RESULT 10  
AAB82775  
ID AAB82775 standard; protein; 13 AA.  
XX  
AC AAB82775;  
XX  
DT 06-AUG-2003 (revised)  
DT 29-OCT-2001 (first entry)

XX Hepatitis B core antigen peptide.  
XX  
KW Telomerase reverse transcriptase; hTERT; human; cytotoxic T lymphocyte;  
KW major histocompatibility complex; cancer; tumour;  
KW human leucocyte antigen; HLA-A2.1; HBVc; vaccine.  
XX  
OS Hepatitis B virus.  
XX  
PN WO200160391-A1.  
XX  
PD 23-AUG-2001.  
XX  
PF 15-FEB-2001; 2001WO-US005143.  
XX  
XX 15-FEB-2000; 2000US-0182685P.  
PR  
PR 15-FEB-2001; 2001US-00182685.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Zanetti M;  
XX  
XX WPI; 2001-536552/59.  
XX  
XX Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,  
PT for treating cancers or tumors or for inducing immune response against  
PT tumors, comprises a telomerase reverse transcriptase peptide.  
XX  
XX Example 1; Page 12; 52pp; English.  
XX  
XX The present sequence is that of a hepatitis B virus core antigen (HBVc)  
CC peptide comprising amino acid residues 128-140. The peptide was used to  
CC immunise HHD mice and results were compared with those obtained using  
CC human telomerase reverse transcriptase (hTERT) HLA-A2.1+ restricted  
CC peptide p540 (see AAB82772). The induction of CTL responses in vitro and  
CC in vivo, and the susceptibility to lysis of tumour cells of various  
CC origins by hTERT CTL suggest that hTERT could serve as a universal cancer  
CC vaccine for humans. A claimed universal vaccine for treating tumours of  
CC any origin comprises at least 1 hTERT peptide. The peptide is 7-15 amino  
CC acid residues in length and may be modified to enhance binding to the  
CC major histocompatibility complex. Also claimed is a method for inducing  
CC and enhancing a CTL response against cancer cells, involving harvesting  
CC blood leucocytes, pulsing with hTERT, and contacting cancer cells with the  
CC pulsed leucocytes. A method for targeting CTL to tumour cells is also  
CC claimed, and involves administering a hTERT peptide to a mammal,  
CC especially a cancer patient. (Updated on 06-AUG-2003 to correct OS  
CC field.)  
XX  
SQ Sequence 13 AA;  
Query Match 100.0%; Score 74; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TPPAYRPPNAPIL 13  
DB 1 TPPAYRPPNAPIL 13  
RESULT 11  
AAUC0614  
ID AAUC0614 standard; peptide; 13 AA.  
XX  
AC AAUC0614;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE H-2 I-Ab-restricted HBV core antigen-derived T helper epitope.  
XX  
XX Human; MUC1; antigenic peptide; major histocompatibility complex; MHC-I;  
KW glycoprotein; cytotoxic T lymphocytes; T cell response; cancer; vaccine;  
KW cancer gene therapy; diagnosis; treatment; inflammatory disorder; HBV;  
KW organ transplant rejection; graft versus host disease.

XX OS Hepatitis B virus.  
 XX PN WO200118035-A2.  
 XX PD 15-MAR-2001.  
 XX PF 07-SEP-2000; 2000WO-EP008761.  
 XX PR 08-SEP-1999; 99GB-00021242.  
 XX PR 10-SEP-1999; 99EP-00402237.  
 XX PR 03-MAR-2000; 2000US-0187215P.  
 XX FA (TRGE ) TRANSGENE SA.  
 XX FA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
 XX PI Taylor-Papadimitriou J, Heukamp LC, Offringa R, Mellief CJM;  
 XX PI Acres B, Thomas M;  
 XX DR WPI; 2001-235187/24.  
 XX PT New antigenic polypeptides of MUC-1 protein which activate cytotoxic T  
 XX PT lymphocyte proteins and their analogs, useful for identifying a major  
 XX PT histocompatibility complex class I restricted T cell response and for  
 XX PT diagnosing cancer.  
 XX PS Example 5; Page 42; 81pp; English.  
 XX CC The sequence represents an H-2 I-Ab-restricted hepatitis B virus (HBV)  
 XX CC core antigen-derived T helper epitope used in testing of human MUC1  
 XX CC polypeptide derivatives through a cytotoxic T lymphocyte (CTL) assay.  
 XX CC Derivative antigenic peptides of MUC1 protein bind at least one major  
 XX CC histocompatibility complex class I (MHC-I) glycoprotein, which activates  
 XX CC cytotoxic T lymphocytes to induce a protective response against tumours.  
 XX CC Diagnosis of cancer involves determining the presence or absence in a  
 XX CC host cell of MHC class I restricted-T cell response to a MUC1 derivative,  
 XX CC where the presence of the MHC class I restricted T cell response  
 XX CC indicates that the host has cancer. Measurement of the level of MHC class  
 XX CC I restricted T cell response is also useful to monitor the severity of  
 XX CC cancer, a larger response indicating a more severe cancer. MUC1  
 XX CC derivatives are useful in cancer therapy and to follow MUC1 specific  
 XX CC immune responses in patients during the course of disease and/or  
 XX CC treatment. MUC1 DNA is useful in cancer gene therapy, vaccination and  
 XX CC diagnosis. Compositions of the sequences are used in vaccines and  
 XX CC treatments against cancer or diseases caused by an immune response, such  
 XX CC as an inflammatory disorder, organ transplant rejection or graft versus  
 XX CC host disease  
 XX SQ Sequence 13 AA;  
 Query Match 100.0%; Score 74; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TPPAYRPPNPAPIL 13  
 Db 1 TPPAYRPPNPAPIL 13  
 RESULT 12  
 AAU70851  
 ID AAU70851 standard; peptide; 13 AA.  
 XX AC AAU70851;  
 XX DT 14-FEB-2002 (first entry)  
 XX DE Hepatitis B virus antigen binding partner #83.  
 XX KW Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;  
 XX KW antiinflammatory; HBV core antigen; HBCAg; HBV E antigen; HBeAg;  
 XX KW B cell mediated processing; T cell proliferation; cytokine production;  
 XX KW immune system response.

XX OS Synthetic.  
 XX PN WO200181421-A2.  
 XX PD 01-NOV-2001.  
 XX PF 20-APR-2001; 2001WO-IB000844.  
 XX PR 21-APR-2000; 2000US-00356605.  
 XX PA (TRIP-) TRIPEP AB.  
 XX PI Sallberg M;  
 XX DR WPI; 2002-055347/07.  
 XX PT Novel peptide that binds to hepatitis B virus core or E antigen, useful  
 XX PT for treating and preventing hepatitis B virus infection.  
 XX PS Example 6; Page 28; 82pp; English.  
 XX CC The invention relates to an isolated or purified peptide (I) which binds  
 XX CC Hepatitis B virus (HBV) core antigen (HBCAg) or HBV E antigen (HBeAg).  
 XX CC (I) is useful for treating or preventing Hepatitis B virus (HBV)  
 XX CC infection, by identifying a subject in need of a molecule that inhibits  
 XX CC HBV infection, and providing the subject with (I). (I) is also useful for  
 XX CC determining the presence of HBV in a biological sample, and for  
 XX CC inhibiting B cell mediated processing and uptake of HBCAg and/or HBeAg,  
 XX CC by determining whether (I) inhibits B cell mediated processing and uptake  
 XX CC of HBCAg and/or HBeAg by performing an assay of T cell proliferation or  
 XX CC cytokine production. (I) is also useful for modulating an immune system  
 XX CC response. (I) is useful as a template for a design of synthetic molecules  
 XX CC including peptides, derivatives or modified peptides, peptidomimetics and  
 XX CC chemicals. (I) is also useful as biotechnological tool, diagnostic  
 XX CC reagent and as active ingredient in pharmaceuticals. (I) is also useful  
 XX CC as detection reagents in conventional immunochemical techniques, as  
 XX CC diagnostic reagents to detect HBV in biological sample, and to determine  
 XX CC the efficacy of an HBV treatment protocol by monitoring the levels of  
 XX CC HBCAg and/or HBeAg during and after treatment. AAU70766-AAU70876  
 XX CC represent Hepatitis B virus (HBV) core antigen (HBCAg) or HBV E antigen  
 XX CC (HBeAg) binding partners as described in the invention  
 XX SQ Sequence 13 AA;  
 Query Match 100.0%; Score 74; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TPPAYRPPNPAPIL 13  
 Db 1 TPPAYRPPNPAPIL 13  
 RESULT 13  
 ABB76787  
 ID ABB76787 standard; peptide; 13 AA.  
 XX AC ABB76787;  
 XX DT 31-MAY-2002 (first entry)  
 XX DE HBV peptide 128-140.  
 XX KW Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;  
 XX KW human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.  
 XX OS Unidentified.  
 XX PN FR2812087-A1.  
 XX PD 25-JAN-2002.  
 XX XX

PF 21-JUL-2000; 2000FR-00009591.  
 XX  
 PR 21-JUL-2000; 2000FR-00009591.  
 XX  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX  
 PI Kostasopoulos K, Tourdot S, Scardino A, Gross DA;  
 XX  
 XX WPI; 2002-189846/25.  
 DR  
 XX Identifying subdominant or cryptic epitopes, useful in immunotherapy of  
 PT cancer and viral infection, comprises testing modified, non-immunogenic  
 PT peptides for induction of cytotoxic T cells.  
 XX  
 XX Example 1; Page 14; 62pp; French.  
 PS  
 XX The present invention relates to subdominant/cryptic epitopes that are  
 CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The  
 CC epitopes or chimeric polypeptides containing them and nucleic acid  
 CC encoding them are useful for preventative or curative immunotherapy of  
 CC cancer and viral infections, particularly where used as vaccines. The  
 CC present peptide was used to illustrate the invention  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 100.0%; Score 74; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TPPAYRPPNAPIL 13  
 Db 1 TPPAYRPPNAPIL 13  
 RESULT 14  
 ABG62860  
 ID ABG62860 standard; peptide; 13 AA.  
 AC  
 AC ABG62860;  
 XX  
 XX 21-AUG-2002 (first entry)  
 DT  
 XX Antigenic domain peptide from a Hepatitis B virus protein.  
 DE  
 XX Ligand/receptor specificity exchanger; antibody; pathogen receptor;  
 XX bacterial infection; viral infection; yeast infection; cancer;  
 KW parasitic infection; fungal infection; proliferation; antibacterial;  
 KW virucide; cytostatic; antifungal; antigenic domain.  
 XX  
 OS Hepatitis B virus.  
 OS  
 PN WO200224887-A2.  
 XX  
 XX 28-MAR-2002.  
 PD  
 XX 19-SEP-2001; 2001WO-IB002327.  
 PF  
 XX 19-SEP-2000; 2000US-00664025.  
 PR  
 XX (TRIP-) TRIPEP AB.  
 PA  
 XX Sallberg M, Flock J;  
 PI  
 XX WPI; 2002-489707/52.  
 DR  
 XX Novel ligand/receptor specificity exchanger that redirects antibodies to  
 PT receptors on pathogen or tumor cell, has specificity domain having ligand  
 PT for receptor, and antigenic domain having epitope of pathogen or toxin.  
 XX  
 PS Claim 14; Page 14; 79pp; English.  
 XX  
 XX The present invention relates to ligand/receptor specificity exchangers  
 CC comprising at least one specificity domain comprising a ligand for a

CC receptor, and at least one antigenic domain joined to the specificity  
 CC domain, where the antigenic domain comprises an epitope of a pathogen or  
 CC toxin. The ligand/receptor specificity exchangers redirect antibodies to  
 CC receptors present on pathogens. They are useful for preventing and  
 CC treating human diseases such as bacterial, viral, yeast, parasitic and  
 CC fungal infections, and cancer. These compositions act by inhibiting  
 CC proliferation of pathogens, or cancer cells. One of the prophylactic  
 CC applications of the ligand/receptor specificity exchangers includes  
 CC coating or crosslinking it to a medical device or implant which include  
 CC implantable medical devices that tend to serve as foci for infection by a  
 CC number of bacterial species. ABG62853-ABG62869 represent antigenic domain  
 CC peptides used in the methods of the present invention  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 100.0%; Score 74; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TPPAYRPPNAPIL 13  
 Db 1 TPPAYRPPNAPIL 13  
 RESULT 15  
 ABP52344  
 ID ABP52344 standard; peptide; 13 AA.  
 XX  
 AC ABP52344;  
 XX  
 DT 17-OCT-2002 (first entry)  
 DT  
 XX TH epitope.  
 DE  
 XX Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;  
 KW tumour; immune response; cancer; vaccine; antibody.  
 XX  
 OS Synthetic.  
 OS  
 PN WO200258728-A2.  
 XX  
 XX 01-AUG-2002.  
 PD  
 XX 28-JAN-2002; 2002WO-GB000354.  
 PF  
 XX 26-JAN-2001; 2001GB-00002145.  
 PR  
 XX (SCAN-) SCANCELL LTD.  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 XX Durrant LG, Parsons T, Robins A;  
 PI  
 XX WPI; 2002-608418/65.  
 DR  
 XX Use of polypeptides and nucleic acids encoding the polypeptides, in  
 PT manufacturing medicament for stimulating a cytotoxic T cell response and  
 PT for preventing or treating cancer, e.g. colorectal, lung, breast or  
 PT ovarian cancer.  
 XX  
 XX Example 11; Page 45; 87pp; English.  
 PS  
 XX The present invention describes the use of a polypeptide (I) in the  
 CC manufacture of a medicament for stimulating a cytotoxic T cell response,  
 CC where (I) comprises a first portion comprising the part of human FC that  
 CC binds to CD64 and a second portion comprising one or more heterologous T  
 CC cell epitopes. Also described is a method of stimulating a cytotoxic T  
 CC cell response in a patient such as a mammal, preferably human, by  
 CC administering (I) to the patient. (I) has cytostatic activity and can be  
 CC used in vaccine production. (I) and the nucleic acid encoding (I) are  
 CC useful in the manufacture of a medicament for stimulating cytotoxic T  
 CC cell response. The medicament is useful for preventing and/or treating  
 CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The  
 CC medicament stimulates cytotoxic and helper T cell responses. The

CC antibodies are useful as vaccines to stimulate helper and cytotoxic T  
CC cell responses. The polypeptides and nucleic acids are useful in  
CC optimising immunisation schedules for enhancing a protective immune  
CC response against cancer. The present sequence represents a TH epitope  
CC which is used in an example from the present invention

XX  
SQ Sequence 13 AA;

Query Match 100.0%; Score 74; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred.No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13  
| | | | | | | | | | | | |  
Db 1 TPPAYRPPNAPIL 13

Search completed: August 9, 2004, 18:34:34  
Job time : 51 secs

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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:33:55 ; Search time 18 Seconds  
(without alignments)  
37.285 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPAYRPNAPIL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 127817

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	13	1	US-08-305-871A-14
2	74	100.0	13	4	US-08-464-496-19
3	74	100.0	13	4	US-08-788-822A-16
4	74	100.0	13	4	US-08-197-484-113
5	74	100.0	13	4	US-09-311-784A-49
6	74	100.0	13	4	US-09-664-945-50
7	74	100.0	13	5	PCT-US92-07218-19
8	74	100.0	13	5	PCT-US95-02121-113
9	74	100.0	13	5	PCT-US95-16415-9
10	55	74.3	10	3	US-08-159-339A-402
11	51	68.9	9	3	US-08-159-339A-393
12	51	68.9	9	4	US-09-311-784A-198
13	45	60.8	12	3	US-08-602-999A-268
14	45	60.8	12	4	US-09-500-124-268
15	44	59.5	10	2	US-08-737-085A-7
16	44	59.5	10	3	US-09-246-258-7
17	44	59.5	10	3	US-09-532-106-7
18	44	59.5	10	4	US-09-839-666-7
19	42	56.8	13	2	US-08-737-085A-20
20	42	56.8	13	3	US-09-246-258-20
21	42	56.8	13	3	US-09-532-106-20
22	42	56.8	13	4	US-08-839-666-20
23	39	52.7	8	2	US-08-737-085A-6
24	39	52.7	8	3	US-09-246-258-6
25	39	52.7	8	3	US-09-532-106-6
26	39	52.7	8	4	US-09-839-666-6
27	38	51.4	11	1	US-08-336-343A-26

28	38	51.4	11	3	US-08-652-877-23	Sequence 23, Appl
29	38	51.4	11	3	US-08-476-515A-23	Sequence 23, Appl
30	38	51.4	12	4	US-09-845-917A-22	Sequence 22, Appl
31	37	50.0	10	1	US-08-477-509B-11	Sequence 11, Appl
32	37	50.0	10	3	US-08-482-085B-11	Sequence 11, Appl
33	37	50.0	10	4	US-09-444-791A-11	Sequence 11, Appl
34	37	50.0	12	4	US-09-428-082B-313	Sequence 313, Appl
35	36	48.6	12	2	US-08-459-568-61	Sequence 61, Appl
36	36	48.6	12	2	US-08-399-411-61	Sequence 61, Appl
37	36	48.6	12	3	US-08-516-859A-61	Sequence 61, Appl
38	36	48.6	12	3	US-09-078-173A-22	Sequence 22, Appl
39	36	48.6	12	4	US-09-586-472-61	Sequence 61, Appl
40	36	48.6	12	4	US-09-528-706-61	Sequence 61, Appl
41	36	48.6	12	4	US-09-428-082B-312	Sequence 312, Appl
42	36	48.6	13	3	US-09-078-173A-23	Sequence 23, Appl
43	35	47.3	10	1	US-08-230-047-11	Sequence 11, Appl
44	35	47.3	11	4	US-09-311-784A-181	Sequence 181, Appl
45	34	45.9	10	3	US-08-602-999A-141	Sequence 141, Appl

#### ALIGNMENTS

RESULT 1  
US-08-305-871A-14  
; Sequence 14, Application US/08305871A  
; Patent No. 5736142  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Gaeta, Federico  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sidney, John  
; APPLICANT: Alexander, Jeffrey L.  
; TITLE OF INVENTION: Alteration of Immune Response Using Pan  
; TITLE OF INVENTION: DR-Binding Peptides  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/305,871A  
; FILING DATE: 14-SEP-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/121,101  
; FILING DATE: 14-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 14137-0062-10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-305-871A-14

Query Match 100.0%; Score 74; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
|||||  
Db 1 TPPAYRPPNAPIL 13

## RESULT 2

US-08-464-496-19  
; Sequence 19, Application US/08464496  
; Patent No. 6322789  
; GENERAL INFORMATION:  
; APPLICANT: Epiimmune, Inc.  
; APPLICANT: Vitello, Maria  
; APPLICANT: Chesnut, Robert  
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL  
; FILE REFERENCE: 39963-20001.13  
; CURRENT APPLICATION NUMBER: US/08/464,496  
; CURRENT FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: 07/935,811  
; PRIOR FILING DATE: 1992-08-26  
; PRIOR APPLICATION NUMBER: 07/874,491  
; PRIOR FILING DATE: 1992-04-27  
; PRIOR APPLICATION NUMBER: 07/827,682  
; PRIOR FILING DATE: 1992-01-29  
; PRIOR APPLICATION NUMBER: 07/749,568  
; PRIOR FILING DATE: 1991-08-26  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: T helper epitope HBC 128-140  
US-08-464-496-19

Query Match 100.0%; Score 74; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
|||||  
Db 1 TPPAYRPPNAPIL 13

## RESULT 3

US-08-788-822A-16  
; Sequence 16, Application US/08788822A  
; Patent No. 6413935  
; GENERAL INFORMATION:  
; APPLICANT: Alexander, Jeffrey L.  
; APPLICANT: Deftrees, Shawn  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Induction of Immune Response Against  
Desired Determinants  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/788,822A  
; FILING DATE: 23-JAN-1997

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/010,510  
; FILING DATE: 24-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 014137-009210US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-788-822A-16

Query Match 100.0%; Score 74; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
|||||  
Db 1 TPPAYRPPNAPIL 13

## RESULT 4

US-08-197-484-113  
; Sequence 113, Application US/08197484  
; Patent No. 6419931  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; APPLICANT: CHESTNUT, Robert W.  
; APPLICANT: SETTE, Alessandro D.  
; APPLICANT: CELIS, Esteban  
; APPLICANT: GRAY, Howard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990

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; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-113

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
DB 1 TTPAYRPPNAPIL 13

RESULT 5
US-09-311-784A-49
; Sequence 49, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39863-20022.01
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US/09/311,784A
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-09-311-784A-49

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTPAYRPPNAPIL 13

RESULT 6
US-09-664-945-50
; Sequence 50, Application US/09664945
; Patent No. 6560842
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
; FILE REFERENCE: TRIPE.007C3
; CURRENT APPLICATION NUMBER: US/09/664,945
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
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; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: SE 9401460
; PRIOR FILING DATE: 1994-04-28
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antigenic domain peptide
US-09-664-945-50

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
DB 1 TTPAYRPPNAPIL 13

RESULT 7
PCT-US92-07218-19
; Sequence 19, Application PC/TUS9207218
; GENERAL INFORMATION:
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Chesnut, Robert W.
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07218
; FILING DATE: 19920826
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-26-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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PCT-US92-07218-19

Query Match 100.0%; Score 74; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00018;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 |||||  
 Db 1 TPPAYRPPNAPIL 13

## RESULT 8

PCT-US95-02121-113  
 ; Sequence 113, Application PC/TUS9502121  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
 ; TITLE OF INVENTION: CTL IMMUNITY  
 ; NUMBER OF SEQUENCES: 153  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/02121  
 ; FILING DATE: 16-FEB-1995  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/197,484  
 ; FILING DATE: 16-FEB-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/935,811  
 ; FILING DATE: 26-AUG-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/874,491  
 ; FILING DATE: 27-APR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/827,682  
 ; FILING DATE: 29-JAN-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/749,568  
 ; FILING DATE: 26-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Parmelee, Steven W.  
 ; REGISTRATION NUMBER: 31,990  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 467-9600  
 ; TELEFAX: (415) 543-5043  
 ; INFORMATION FOR SEQ ID NO: 113:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 13 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; PCT-US95-02121-113

Query Match 100.0%; Score 74; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00018;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 |||||  
 Db 1 TPPAYRPPNAPIL 13

## RESULT 9

PCT-US95-16415-9  
 ; Sequence 9, Application PC/TUS9516415  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Scripps Research Institute

; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC  
 ; TITLE OF INVENTION: CYTOTOXIC T CELLS  
 ; NUMBER OF SEQUENCES: 38  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: The Scripps Research Institute  
 ; STREET: 10666 North Torrey Pines Road, TPC-8  
 ; CITY: La Jolla  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/16415  
 ; FILING DATE: 13-DEC-1995  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/355,558  
 ; FILING DATE: 14-DEC-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Logan, April C.  
 ; REGISTRATION NUMBER: 33,950  
 ; REFERENCE/DOCKET NUMBER: 433.1PC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 554-2937  
 ; TELEFAX: (619) 554-6312  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 13 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; PCT-US95-16415-9

Query Match 100.0%; Score 74; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00018;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
 |||||  
 Db 1 TPPAYRPPNAPIL 13

## RESULT 10

US-08-159-339A-402  
 ; Sequence 402, Application US/08159339A  
 ; Patent No. 6037135  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kubo, Ralph T.  
 ; APPLICANT: Grey, Howard M.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Celis, Esteban  
 ; TITLE OF INVENTION: HLA Binding peptides and Their  
 ; TITLE OF INVENTION: Uses  
 ; NUMBER OF SEQUENCES: 1254  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/159,339A  
 ; FILING DATE: 29-NOV-1993



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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 402:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-402

Query Match 74.3%; Score 55; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AYRPPNAPIL 13
DB 1 AYRPPNAPIL 10

RESULT 11
US-08-159-339A-393
; Sequence 393, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cells, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-393

Query Match 68.9%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AYRPPNAPI 12
DB 1 AYRPPNAPI 9

RESULT 12
US-09-311-784A-198
; Sequence 198, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 198
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV NUC 131 (peptide 1090.02)
; US-09-311-784A-198

Query Match 68.9%; Score 51; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AYRPPNAPI 12
DB 1 AYRPPNAPI 9

RESULT 13
US-08-602-999A-268
; Sequence 268, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

```

```

/ TITLE OF INVENTION: ISOLATING AND USING SAME
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/602,999A
/ FILING DATE: 16-FEB-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mistrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-202
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 268:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-09-500-124-268

Query Match 60.8%; Score 45; DB 3; Length 12;
Best Local Similarity 63.6%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPAYRPPNAPI 12
||| |||
Db 2 PPAYPPPPVPV 12
||| |||

RESULT 14
US-09-500-124-268
/ Sequence 268, Application US/09500124
/ Patent No. 6432920
/ GENERAL INFORMATION:
/ APPLICANT: SPARKS, Andrew B.
/ APPLICANT: KAY, Brian K.
/ APPLICANT: THORN, Judith M.
/ APPLICANT: QUILLIAM, Lawrence A.
/ APPLICANT: DER, Channing J.
/ APPLICANT: FOWLES, Dana M.
/ APPLICANT: RIDER, James E.
/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
/ ISOLATING AND USING SAME
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/500,124
/ FILING DATE:

Query Match 60.8%; Score 45; DB 3; Length 12;
Best Local Similarity 63.6%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPAYRPPNAPI 12
||| |||
Db 2 PPAYPPPPVPV 12
||| |||

RESULT 15
US-08-737-085A-7
/ Sequence 7, Application US/08737085A
/ Patent No. 5869232
/ GENERAL INFORMATION:
/ APPLICANT: SALLBERG, MATTI
/ TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
/ EXCHANGER
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DARBY & DARBY PC
/ STREET: 805 Third Avenue
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/737,085A
/ FILING DATE: 27-DEC-1996
/ CLASSIFICATION: 426
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Green, Reza
/ REGISTRATION NUMBER: 38,475
/ REFERENCE/DOCKET NUMBER: 3846/0C569
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-527-7659
/ TELEX: 212-753-6237
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-737-085A-7

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Query Match 59.5%; Score 44; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. NO. 1.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 RPPNAPIL 13  
Db 1 RPPNAPIL 8

Search completed: August 9, 2004, 18:36:38  
Job time : 19 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2004, 18:35:46 ; Search time 40 Seconds  
(without alignments)  
101.947 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 31362936 residues

Total number of hits satisfying chosen parameters: 189912

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	13	9	US-09-839-447A-86
2	74	100.0	13	10	US-09-277-074-9
3	74	100.0	13	12	US-09-277-064-9
4	74	100.0	13	12	US-10-371-525-49
5	74	100.0	13	12	US-10-372-735-55
6	74	100.0	13	12	US-10-182-252A-1374
7	74	100.0	13	12	US-10-333-430-63
8	74	100.0	13	12	US-09-788-110A-4
9	74	100.0	13	12	US-09-055-744-10
10	74	100.0	13	13	US-10-106-487-22
11	74	100.0	13	14	US-10-128-711-113
12	74	100.0	13	14	US-10-116-118-30
13	74	100.0	13	15	US-10-371-069-49
14	74	100.0	13	15	US-10-371-645-43
15	74	100.0	13	15	US-10-371-260-49

Sequence 86, Appl  
Sequence 22, Appl  
Sequence 50, Appl  
Sequence 600, Appl  
Sequence 599, Appl  
Sequence 613, Appl  
Sequence 586, Appl  
Sequence 587, Appl  
Sequence 598, Appl  
Sequence 612, Appl  
Sequence 626, Appl  
Sequence 585, Appl  
Sequence 379, Appl  
Sequence 584, Appl  
Sequence 311, Appl  
Sequence 370, Appl  
Sequence 597, Appl  
Sequence 611, Appl  
Sequence 625, Appl  
Sequence 639, Appl  
Sequence 198, Appl  
Sequence 198, Appl  
Sequence 198, Appl  
Sequence 198, Appl  
Sequence 596, Appl  
Sequence 610, Appl  
Sequence 624, Appl  
Sequence 638, Appl  
Sequence 651, Appl  
Sequence 583, Appl

# ALIGNMENTS

RESULT 1  
US-09-839-447A-86  
; Sequence 86, Application US/09839447A  
; Patent No. US20020058247A1  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; FILE REFERENCE: TRIPEP.020CP1  
; CURRENT APPLICATION NUMBER: US/09/839,447A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/556605  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-09-839-447A-86

Query Match 100.0%; Score 74; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13  
Db 1 TPPAYRPPNAPIL 13

RESULT 2  
US-09-277-074-9  
; Sequence 9, Application US/09277074  
; Publication No. US2003002820A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, Linda A.

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; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR21558
; CURRENT APPLICATION NUMBER: US/09/277,074
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
; OTHER INFORMATION: Artificially Synthesized Peptides
US-09-277-074-9

Query Match 100.0%; Score 74; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 3
US-09-277-064-9
; Sequence 9, Application US/09277064
; Publication No. US20030064916A1
; GENERAL INFORMATION:
; APPLICANT: Sherzhan, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR21525
; CURRENT APPLICATION NUMBER: US/09/277,064
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
; OTHER INFORMATION: Artificially Synthesized Peptides
US-09-277-064-9

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 4
US-10-371-525-49.
; Sequence 49, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fites, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39563-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
```

```
; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-525-49

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 5
US-10-372-735-55
; Sequence 55, Application US/10372735
; Publication No. US20030225251A1
; GENERAL INFORMATION:
; APPLICANT: Salberg, Matti
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; FILE REFERENCE: TRIPEP.7AUC4CP1
; CURRENT APPLICATION NUMBER: US/10/372,735
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/234,579
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: PCT/SE95/00468
; PRIOR FILING DATE: 1995-04-27
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/664,025
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: PCT/IB01/02327
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 10/153,271
; PRIOR FILING DATE: 2002-05-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptides
US-10-372-735-55

Query Match 100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13
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```

RESULT 6
US-10-182-252A-1374
; Sequence 1374, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PC/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1374
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-182-252A-1374

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPPAYRPPNAPIL 13
DB      1 TPPAYRPPNAPIL 13

RESULT 7
US-10-333-430-63
; Sequence 63, Application US/10333430
; Publication No. US2004007240A1
; GENERAL INFORMATION:
; APPLICANT: INSERM
; APPLICANT: INSTITUT GUSTAVE ROUSSY
; APPLICANT: KOSMATOPOULOS, Kostas
; APPLICANT: TOURDOT, Sophie
; APPLICANT: SCARDINO, Antonio
; APPLICANT: GROSS, David, Alexandre
; TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
; TITLE OF INVENTION: IMMUNOTHERAPY
; FILE REFERENCE: 33339/259034
; CURRENT APPLICATION NUMBER: US/10/333,430
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: FR 0003591
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-333-430-63

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPPAYRPPNAPIL 13
DB      1 TPPAYRPPNAPIL 13

RESULT 8
US-09-788-110A-4
; Sequence 4, Application US/09788110A
; Publication No. US20040086518A1
; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; TITLE OF INVENTION: Telomerase Reverse Transcriptase
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-110A-4

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPPAYRPPNAPIL 13
DB      1 TPPAYRPPNAPIL 13

RESULT 9
US-09-055-744-10
; Sequence 10, Application US/09055744
; Publication No. US20010019714A1
; GENERAL INFORMATION:
; APPLICANT: Sia, Charles
; APPLICANT: Chong, Pele
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: HIV-SPECIFIC CYTOTONIX T-CELL RESPONSES
; FILE REFERENCE: 1038-746
; CURRENT APPLICATION NUMBER: US/09/055,744
; CURRENT FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-055-744-10

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPPAYRPPNAPIL 13
DB      1 TPPAYRPPNAPIL 13

RESULT 10
US-10-106-487-22
; Sequence 22, Application US/10106487
; Publication No. US20020164721A1
; GENERAL INFORMATION:
; APPLICANT: FIRAT, HUSEYIN
; APPLICANT: LENONNIER, FRANCOIS
; APPLICANT: LANGLADE-DEMOYEN, PIERRE
; APPLICANT: MICHEL, MARIE-LOUISE
; TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION
; TITLE OF INVENTION: OF
; TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING
US-10-106-487-22

Query Match      100.0%; Score 74; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPPAYRPPNAPIL 13
DB      1 TPPAYRPPNAPIL 13
```

```
; TITLE OF INVENTION: HHD MICE
; FILE REFERENCE: 03495.0196 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/106,487
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/675,673
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/158,356
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-106-487-22

Query Match 100.0%; Score 74; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 11
US-10-128-711-113
; Sequence 113, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 113:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-128-711-113

Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 12
US-10-116-118-30
; Sequence 30, Application US/10116118
; Publication No. US20030143672A1
; GENERAL INFORMATION:
; APPLICANT: Targri, Shabnam
; APPLICANT: Sette, Alessandro
; APPLICANT: Fikes, John D.
; APPLICANT: Ishioka, Glenn
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.0090003
; CURRENT APPLICATION NUMBER: US/10/116,118
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/166,529
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: US 60/239,008
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: (HBV core)
US-10-116-118-30

Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 13
US-10-371-069-49
; Sequence 49, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
```



```
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-069-49

Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13
|||||
|

RESULT 14
US-10-371-645-49
; Sequence 49, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-645-49

Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13
|||||
|

RESULT 15
US-10-371-260-49
; Sequence 49, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-260-49

Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13
|||||
|

RESULT 16
US-10-371-260-49
; Sequence 49, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-260-49

Query Match      100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13
|||||
|

Search completed: August 9, 2004, 18:41:00
Job time : 40 secs
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:31:10 ; Search time 16 Seconds  
(without alignments)  
78.156 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPPAYRPPNAPI 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1827

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	39.2	11	1 XAVIDH	bradykinin-potenti
2	29	39.2	12	2 S71380	lebetin 1 isoform
3	29	39.2	13	2 S21152	tryptophyllin-rela
4	29	39.2	13	2 S09716	2S albumin large c
5	24	32.4	13	2 G37266	IG heavy chain C r
6	23	31.1	9	2 A61358	bradykinin-like pe
7	23	31.1	9	2 A61057	Thr-6 bradykinin -
8	23	31.1	9	2 A26744	bradykinin-like pe
9	23	31.1	9	2 A61363	bradykinin - commo
10	23	31.1	9	2 A60579	bradykinin-like pe
11	23	31.1	9	2 B60246	ornitho-kinin - ch
12	23	31.1	9	2 S65433	bradykinin - horn
13	23	31.1	9	2 A43065	hydroxyproline-3-b
14	23	31.1	11	2 A61365	pyllokinin - Rohd
15	23	31.1	11	2 B26744	megascollakinin -
16	23	31.1	11	2 S13279	Ile-Ser-bradykinin
17	23	31.1	12	2 A61360	vespakinin M - hor
18	23	31.1	12	2 A61359	vespakinin X - hor
19	23	31.1	13	2 A61361	bradykinin-like pe
20	22	29.7	10	2 S39030	lysyl-bradykinin -
21	22	29.7	11	2 I33098	173K exoantigen -
22	22	29.7	12	2 P00046	ATP synthase D cha
23	22	29.7	12	2 B39690	neural cell adhesi
24	22	29.7	13	2 D39690	neural cell adhesi
25	22	29.7	13	2 A05174	tryptophyllin-13 -
26	21	28.4	7	2 A61081	tryptophyllin, bas
27	21	28.4	10	2 S26505	collagen alpha 1(V
28	20	27.0	8	2 B39745	endoglycosylcerami
29	20	27.0	9	2 P40139	carbon-monoxide de

#### ALIGNMENTS

##### RESULT 1

XAVIDH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 05-Aug-1994

C;Accession: JC0002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Accession: JC0002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyrog

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 39.2%; Score 29; DB 1; Length 11;

Best Local Similarity 71.4%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 RPPNAPI 12

DB 3 RPPGPP 9

##### RESULT 2

S71380

lebetin 1 isoform beta - Vipera lebetina

C;Species: Vipera lebetina

C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C;Accession: S71380

R;Barbouche, R.; Marrakchi, N.; Mansuelle, P.; Krifi, M.; Fenouillet, E.; Rochat, H.; El

PEBS Lett 392, 6-10, 1996

A;Title: Novel anti-platelet aggregation polypeptides from Vipera lebetina venom: isolat

A;Reference number: S71379; MUID:96354866; PMID:8769304

A;Accession: S71380

A;Molecule type: protein

A;Residues: 1-12 <BAR>

A;Experimental source: venom

C;Keywords: anticoagulant; venom

Query Match 39.2%; Score 29; DB 2; Length 12;

Best Local Similarity 62.5%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPAYRPPN 9

DB 4 PPKKGPPN 11

```

RESULT 3
S21152
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S21152
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Palconieri Erspaner, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of th
A:Reference number: S21152; PMID:92339502; PMID:1633846
A:Accession: S21152
A:Molecule type: protein
A:Residues: 1-13 <MIG>
A:Experimental source: skin
C:Superfamily: unassigned animal peptides

Query Match 39.2%; Score 29; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PAYRPPNAPI 12
DB 4 PFYPPPIYPV 13

RESULT 4
S09716
C:Species: Brassica napus (rape)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C:Accession: S09716; S09718; S09717
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; PMID:90242974; PMID:2185951
A:Accession: S09716
A:Molecule type: protein
A:Residues: 1-9; 10-13 <MON>
A:Experimental source: seed
A:Note: 3-Ser was also found
A:Accession: S09718
A:Molecule type: protein
A:Residues: 1-9; 10-13 <MO2>
A:Experimental source: seed
A:Accession: S09717
A:Molecule type: protein
A:Residues: 1-9; 10-13 <MO3>
A:Experimental source: seed

Query Match 39.2%; Score 29; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PAYRPPNAP 11
DB 4 PQRRPPPGP 12

RESULT 5
G37266
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: G37266
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; PMID:91177923; PMID:1706720
A:Accession: G37266
A>Status: preliminary
A:Molecule type: mRNA

```

A;Residues: 1-13 <RUF>

Query Match 32.4%; Score 24; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 8.1e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPPAYRP 7  
DB 4 TPSPQVP 10

#### RESULT 6

A61358  
C:Species: Rana nigromaculata (Japanese pond frog)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 02-Sep-2000  
C:Accession: A61358  
R:Nakajima, T.  
Chem. Pharm. Bull. 16, 769-770, 1968  
A:Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin  
A:Reference number: A61358; PMID:68412013; PMID:5677638  
A:Accession: A61358  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <NAK>  
C:Superfamily: unassigned animal peptides  
C:Keywords: skin

Query Match 31.1%; Score 23; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7  
DB 2 PGFTTP 7

#### RESULT 7

A61057  
C:Species: Colpa interrupta  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Aug-2000  
C:Accession: A61057  
R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.  
Comp. Biochem. Physiol. C 96, 157-162, 1990  
A:Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynapt  
A:Reference number: A61057; PMID:91130217; PMID:1980872  
A:Accession: A61057  
A:Molecule type: protein

A;Residues: 1-9 <PIB>  
C:Superfamily: unassigned animal peptides  
C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 31.1%; Score 23; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7  
DB 2 PGFTTP 7

#### RESULT 8

A26744  
C:Species: Thre-6-bradykinin  
N:Alternate names: Thre-6-bradykinin  
C:Species: Megascollia flavifrons (garden dagger wasp)  
C:Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 18-Aug-2000  
C:Accession: A26744  
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.  
Toxicol 25, 527-535, 1987  
A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp  
A:Reference number: A94322; PMID:87293024; PMID:3617088

A;Accession: A26744  
 A;Molecule type: protein  
 A;Residues: 1-9 <YAS>  
 C;Superfamily: unassigned animal peptides

Query Match 31.1%; Score 23; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PPAYRP 7  
 || : |  
 Db 2 PPGFTP 7

## RESULT 9

A61363  
 bradykinin - common frog  
 C;Species: Rana temporaria (common frog)  
 C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
 C;Accession: A61363  
 R;Anastasi, A.; Erspamer, V.; Bertaccini, G.  
 Comp. Biochem. Physiol. A 14, 43-52, 1965  
 A;Title: Occurrence of bradykinin in the skin of Rana temporaria.  
 A;Reference number: A61363  
 A;Accession: A61363  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <AWA>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: skin

Query Match 31.1%; Score 23; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PPAYRP 7  
 || : |  
 Db 2 PPGFTP 7

## RESULT 10

A60579  
 bradykinin-like peptide - slider turtle  
 C;Species: Pseudemys scripta (slider)  
 C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
 C;Accession: A60579  
 R;Conlon, J.M.; Hicks, J.W.; Smith, D.D.  
 Endocrinology 126, 985-991, 1990  
 A;Title: Isolation and biological activity of a novel kinin ([Thr(6)]bradykinin) from the  
 A;Reference number: A60579; PMID:2298179  
 A;Accession: A60579  
 A;Molecule type: protein  
 A;Residues: 1-9 <CON>  
 C;Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammalian  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: plasma

Query Match 31.1%; Score 23; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PPAYRP 7  
 || : |  
 Db 2 PPGFTP 7

## RESULT 11

B60246  
 ornitho-kinin - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 18-Aug-2000  
 C;Accession: B60246  
 R;Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.

Adv. Exp. Med. Biol. 247A, 359-367, 1989  
 A;Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemical  
 A;Reference number: A60246; PMID:90102072; PMID:2603803  
 A;Accession: B60246  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <KIM>  
 C;Superfamily: unassigned animal peptides

Query Match 31.1%; Score 23; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PPAYRP 7  
 || : |  
 Db 2 PPGFTP 7

## RESULT 12

S65433  
 bradykinin - horn fly (fragment)  
 C;Species: Haematobia irritans (horn fly)  
 C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
 C;Accession: S65433  
 R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P.  
 Eur. J. Biochem. 237, 414-423, 1996  
 A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran  
 A;Reference number: S65431; PMID:96215437; PMID:8647080  
 A;Accession: S65433  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <WIJ>  
 A;Note: the source is designated as Haematobia irritans exigua

Query Match 31.1%; Score 23; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PPAYRP 7  
 || : |  
 Db 2 PPGFTP 7

## RESULT 13

A43065  
 hydroxyproline-3-bradykinin - frog (Helleophryne purcelli)  
 C;Species: Helleophryne purcelli  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
 C;Accession: A43065  
 R;Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.  
 Experientia 35, 1133, 1979  
 A;Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South A  
 A;Reference number: A43065; PMID:80024576; PMID:488255  
 A;Accession: A43065  
 A;Molecule type: protein  
 A;Residues: 1-9 <NAK>  
 C;Keywords: bradykinin; hydroxyproline; skin  
 F;3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 31.1%; Score 23; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PPAYRP 7  
 || : |  
 Db 2 PPGFTP 7

## RESULT 14

A61365  
 phyllokinin - Rohde's leaf frog  
 N;Alternate names: bradykinyl-tyrosine O-sulfate  
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C>Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
 C/Accession: A61365  
 R/Anastasi, A.; Bertaccini, G.; Erspamer, V.  
 Br. J. Pharmacol. 27, 479-485, 1966  
 A/Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate)  
 A/Reference number: A61365; MUID:67179312; PMID:5970899

A/Accession: A61365  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-11 <ANA>  
 C/Superfamily: unassigned animal peptides  
 C/Keywords: sulfoprotein  
 F/11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 31.1%; Score 23; DB 2; Length 11;  
 Best Local Similarity 50.0%; Pred.No. 9.5e+02;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7  
 DB 2 PPGFSP 7

## RESULT 15

B26744  
 megascaliakinin - garden dagger wasp  
 N/Alternate names: 6-Thr-bradykinin-Lys-Ala  
 C/Species: Megascalia flavifrons (garden dagger wasp)  
 C/Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 18-Aug-2000  
 C/Accession: B26744; A28609  
 R/Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.  
 Toxicon 25, 527-535, 1987  
 A/Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp  
 A/Reference number: A94322; MUID:87293024; PMID:3617088  
 A/Accession: B26744  
 A/Molecule type: protein  
 A/Residues: 1-11 <YAS>  
 R/Nakajima, T.; Piek, T.; Yasuhara, T.; Mantel, P.  
 Toxicon 26, 34, 1988  
 A/Title: Two kinins isolated from the venom of Megascalia flavifrons.  
 A/Reference number: A28609  
 A/Accession: A28609  
 A/Molecule type: protein  
 A/Residues: 1-11 <NAK>  
 C/Superfamily: unassigned animal peptides  
 C/Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 31.1%; Score 23; DB 2; Length 11;  
 Best Local Similarity 50.0%; Pred.No. 9.5e+02;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7  
 DB 2 PPGFSP 7

Search completed: August 9, 2004, 18:36:09  
 Job time : 17 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:29:25 ; Search time 13 Seconds  
(without alignments)  
52.070 Million cell updates/sec

Title: US-09-277-074-9  
Perfect score: 74  
Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues 597  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29	39.2	11	1 BPP_AKGHP	P04562 agkistrodon
2	24	32.4	7	1 TPFF_PACDA	P83455 pachymedusa
3	23	31.1	8	1 PKP2_PERAM	P82692 periplaneta
4	23	31.1	9	1 KNL3_BOMVA	P83058 bombina var
5	23	31.1	11	1 BRK_MEGFL	P12797 megascalia
6	23	31.1	12	1 GRAR_RANRU	P40754 rana rugosa
7	23	31.1	13	1 BRK_PARID	P42717 parapolybia
8	22	29.7	10	1 BRK_ONCMY	Q9PZ1 oncothynchu
9	22	29.7	13	1 TV13_PHYRO	P04096 phyllomedus
10	20	27.0	6	1 OVM_LEPDE	P42985 leptinotars
11	20	27.0	10	1 TMOF_AEDAE	P19425 aedes aegypt
12	19	25.7	9	1 NEUF_CAVPO	P34966 cavia porce
13	19	25.7	10	1 BPP8_BOTIN	P30426 bothrops in
14	19	25.7	10	1 URE3_NORMO	P17339 morganelia
15	19	25.7	12	1 FARI_CALVO	P41869 calliphora
16	19	25.7	12	1 TAL0_TREME	P01371 tremella me
17	18	24.3	12	1 FAR7_PENMO	P83322 penaeus mon
18	18	24.3	13	1 BLAC_STRGR	P81173 streptomyc
19	17	23.0	7	1 MNE1_LEPDE	P42984 leptinotars
20	17	23.0	7	1 UF04_MOUSE	P38642 mus musculu
21	17	23.0	9	1 ISOT_CYPCA	P42993 cyprinus ca
22	17	23.0	9	1 OXYT_OCTVU	P80027 octopus vul
23	17	23.0	11	1 BPP3_BOTIN	P30423 bothrops in
24	17	23.0	11	1 BPP4_BOTIN	P30424 bothrops in
25	17	23.0	11	1 BPPB_AKGHA	P01021 agkistrodon
26	17	23.0	11	1 TKM1_UPEIN	P82026 uperoleia i
27	17	23.0	11	1 TKM1_UPERU	P08612 uperoleia r
28	17	23.0	13	1 ADFB_TENMO	P83109 tenebrio mo
29	16	21.6	9	1 OXYA_SCYCA	P42996 scylliorhinu
30	16	21.6	9	1 OXYF_SCYCA	P42997 scylliorhinu
31	16	21.6	9	1 OXVV_SQUAC	P43000 squalus aca
32	16	21.6	10	1 ESTA_SCHGA	P81012 schizaphis
33	16	21.6	10	1 LPK2_LOCMI	P41488 locusta mig

ALIGNMENTS

RESULT 1

BPP\_AKGHP STANDARD; PRT; 11 AA.  
AC P04562; 13 21.6 16 MPI\_MICOC  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys  
OS pallas).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_TaxID=8714;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom; PubMed=3008123;  
RX MEDLINE=86177022; Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;  
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;  
RT "Structure-function studies on the bradykinin potentiating peptide  
RT from Chinese snake venom (Agkistrodon halys pallas).";  
RL Peptides 6 Suppl. 3:339-342(1985).  
CC -/- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; JC0002; XAVIBH.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 39.2%; Score 29; DB 1; Length 11;  
Best Local Similarity 71.4%; Pred. No. 81;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 RPPNAPI 12  
Db 3 RPPGPPI 9

RESULT 2

TPFF\_PACDA STANDARD; PRT; 7 AA.  
AC P83455;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tryptophyllin-1 (pdt-1).  
OS Pachymedusa dactylosa (Giant mexican leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Phyllomedusinae; Pachymedusa.  
OX NCBI\_TaxID=75988;  
RN [1]  
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF

PRO-7.  
RC TISSUE=Skin secretion;  
RA Chen T.B., Orr D.F., Shaw C.;  
RT "Pachymedusa danielcolor tryptophyllin-1 (Pdt-1): structural  
characterization, pharmacological activity and cloning of precursor  
cDNA";  
RL Submitted (SEP-2002) to Swiss-Prot.  
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
smooth muscle.  
CC -!- SURCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.  
KW Amphibian defense peptide; Amidation; Hydroxylation.  
FT MOD\_RES 3  
FT MOD\_RES 7  
FT MOD\_RES 8  
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;  
  
Query Match 32.4%; Score 24; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 PPAYRP 7  
DB 2 PPWVP 7  
  
RESULT 3  
ID PKK2\_PPRAM STANDARD; PRT; 8 AA.  
AC P82692;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=97353923; PubMed=9210163;  
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
RT Isolation and structural elucidation of two pyrokinins from the  
retrocerebral complex of the American cockroach.;  
RL Peptides 18:473-478 (1997).  
RN [2]  
TISSUE SPECIFICITY.  
RP MEDLINE=20189894; PubMed=10723010;  
RX Predel R., Eckert M.;  
RA "Tagma-specific distribution of FXPRLamides in the nervous system of  
the American cockroach";  
RL J. Comp. Neurol. 419:352-363 (2000).  
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
activity).  
CC -!- TISSUE SPECIFICITY: Corpora cardiaca.  
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
CC -!- SIMILARITY: Belongs to the pyrokinin family.  
DR InterPro: IPR001484; Pyrokinin.  
DR PROSITE: PS00539; PYROKININ; FALSE\_NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 8  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;  
  
Query Match 31.1%; Score 23; DB 1; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 7 PPNAPIL 13  
||| |

Db 2 PPFAPRL 8  
  
RESULT 4  
ID KNL3\_BOMVA STANDARD; PRT; 9 AA.  
AC P83058;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE [Thr6]bradykinin.  
OS Bombina variegata (Yellow-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_TaxID=8348;  
RN [1]  
SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.  
RC TISSUE=Skin secretion;  
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;  
RT Cloning and post-translational processing of frog skin kininogens.;  
RL Submitted (JUL-2001) to Swiss-Prot.  
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat  
arterial smooth muscle and constriction of intestinal smooth  
muscle.  
CC -!- SURCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the bradykinin family.  
KW Amphibian defense peptide; Vasodilator; Bradykinin.  
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;  
  
Query Match 31.1%; Score 23; DB 1; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 PPAYRP 7  
DB 2 PPGTTP 7  
  
RESULT 5  
ID BRK\_MEGFL STANDARD; PRT; 11 AA.  
AC P12797;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Megascolikinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like  
peptide ([Thr6]bradykinin)].  
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Scolidae; Megascolia.  
OX NCBI\_TaxID=7437;  
RN [1]  
SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=87293024; PubMed=3617088;  
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;  
RT "Two kinins isolated from an extract of the venom reservoirs of the  
solitary wasp Megascolia flavifrons.";  
RL Toxicol 25:527-535 (1987).  
RN [2]  
SEQUENCE.  
RC TISSUE=Venom;  
RX "Two kinins isolated from the venom of Megascolia flavifrons.";  
RA Nakajima T., Piek T., Yasuhara T., Mantel P.;  
RL Toxicol 26:34-34 (1988).  
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower  
activities (e.g. smooth muscle contraction).  
CC -!- SURCELLULAR LOCATION: Secreted; wasp venom reservoirs.  
CC -!- SIMILARITY: Belongs to the bradykinin family.  
DR PIR: B26744; B26744.  
DR GO: GO:0005615; C:extracellular space; IDA.



DR GO: 0045776; P: negative regulation of blood pressure; ISS.  
DR GO: 0045987; P: positive regulation of smooth muscle contracta. . . ; TAS.  
KW Bradykinin; Vasodilator.  
FT PEPTIDE 1 11 MEGASCOLIAXININ.  
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.  
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 31.1%; Score 23; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7  
DB 2 PPGTTP 7

RESULT 6  
ID GRAR\_RANRU STANDARD; PRT; 12 AA.  
AC P40754;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Granuliberin-R.  
OS Rana rugosa (wrinkled frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8410;  
RN [1]  
RP TISSUE=Skin secretion;  
RC MEDLINE=78062810; PubMed=589733;  
RA Nakajima T., Yasuhara T.;  
RT "A new mast cell degranulating peptide, granuliberin-R, in the frog  
RL Chem. Pharm. Bull. 25:2464-2465 (1977).  
RN [2]

RP SYNTHESIS.  
RX MEDLINE=78189201; PubMed=657408;  
RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,  
RA Koyama K., Yajima H.;  
RT "Synthesis of the dodecapeptide amide corresponding to the entire  
RT amino acid sequence of granuliberin-R, a new frog skin peptide from  
RT Rana rugosa.";  
RL Chem. Pharm. Bull. 26:1222-1230 (1978).  
CC -!- FUNCTION: Mast cell degranulating peptide.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Mast cell degranulation; Amidation.  
FT MOD\_RES 12 12 AMIDATION.  
SQ SEQUENCE 12 AA; 1424 MW; 23974EB9CA1B5047 CRC64;

Query Match 31.1%; Score 23; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PAYRPP 8  
DB 5 PIYRRP 10

RESULT 7  
ID BRK\_PARID STANDARD; PRT; 13 AA.  
AC P42717;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Waspskinin.  
OS Parapolybia indica.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Polistinae; Parapolybia.

OX NCBI\_TaxID=31921;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Toki T., Yasuhara T., Nakajima T.;  
RT "Isolation and sequential analysis of peptides on the venom sac of  
RT Parapolybia indica.";  
RL Eisei Dobutsu 39:105-111 (1998).  
CC -!- FUNCTION: Induces smooth muscle contraction.  
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.  
CC -!- SIMILARITY: Belongs to the bradykinin family.  
KW Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 13 AA; 1573 MW; 2673CB3D93ECC867 CRC64;

Query Match 31.1%; Score 23; DB 1; Length 13;  
Best Local Similarity 50.0%; Pred. No. 7e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7  
DB 5 PPGFSP 10

RESULT 8  
ID BRK\_ONCMY STANDARD; PRT; 10 AA.  
AC Q9PRZ1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lysyl-bradykinin-like.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94039817; PubMed=8224232;  
RA Conlon J.M., Olson K.R.;  
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from  
RT trout plasma.";  
RL FEBS Lett. 334:75-78 (1993).  
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR  
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Plasma.  
CC -!- SIMILARITY: Belongs to the bradykinin family.  
DR PIR; S39030; S39030.  
KW Bradykinin; Vasodilator.  
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 29.7%; Score 22; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 7.4e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7  
DB 3 PPGWSP 8

RESULT 9  
ID TV13\_PHYRO STANDARD; PRT; 13 AA.  
AC P04056;  
DT 01-NOV-1986 (Rel. 03, Created)  
DT 01-NOV-1986 (Rel. 03, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tryptophyllin-13.  
OS Phyllomedusa rohdei (Rohde's leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Xyloidea; Hylidae;

Query Match 25.7%; Score 19; DB 1; Length 9;

Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 YRPN 9  
: || |  
Db 5 FRPN 9

RESULT 13  
BPP8\_BOTIN STANDARD; PRT; 10 AA.  
ID BPP8\_BOTIN  
AC P30426;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting  
enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
angiotensin-converting enzyme and enhances the action of  
bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; H37196; H37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1  
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 25.7%; Score 19; DB 1; Length 10;  
Best Local Similarity 75.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PNAP 11  
: || |  
Db 6 PNIP 9

RESULT 14  
URE3\_MORNO STANDARD; PRT; 10 AA.  
ID URE3\_MORNO  
AC P17339;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)  
DE (Urease 6 kDa subunit) (Fragment).  
GN UREA.  
OS Morganella morganii (Proteus morganii).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Morganella.  
OX NCBI\_TaxID=582;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90264298; PubMed=2345135;  
RA Hu L.-T., Nicholson B.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
RT "Morganella morganii urease: purification, characterization, and  
isolation of gene sequences.";  
RL J. Bacteriol. 172:3073-3080(1990).  
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
CC -!- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: Belongs to the urease gamma subunit family.

DR PIR; C35389; C35389.  
DR HAMAP; MF\_00739; -; 1.  
KW Hydrolase.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 25.7%; Score 19; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPP 3  
: || |  
Db 4 TPP 6

RESULT 15  
PARI\_CALVO STANDARD; PRT; 12 AA.  
ID PARI\_CALVO  
AC P41889;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Callimyrinamide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duvé H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Renfield J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
neuropeptides (designated callimyrinamides) from the blowfly  
Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
family.  
DR PIR; E44787; E44787.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 12 12  
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match 25.7%; Score 19; DB 1; Length 12;  
Best Local Similarity 75.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PNAP 11  
: || |  
Db 2 PNQP 5

Search completed: August 9, 2004, 18:34:58  
Job time : 14 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 9, 2004, 18:30:25 ; Search time 34 Seconds  
(without alignments)  
120.639 Million cell updates/sec

Title: US-09-277-074-9

Perfect score: 74

Sequence: 1 TPPAYRPPNAPIL 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3001

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*  
1: sp archea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	35.1	11	11 Q80W11	Q80w11 mus sp. nt-
2	25	33.8	10	4 Q3UE86	Q3ue86 homo sapien
3	23	31.1	12	13 Q3PWS5	Q3pws5 gallus gall
4	22	29.7	9	4 Q9UCS8	Q9ucs8 homo sapien
5	22	29.7	9	10 P82429	P82429 nicotiana t
6	22	29.7	9	13 Q9PRJ4	Q9prj4 lepisosteus
7	21.5	29.1	12	10 P82441	P82441 nicotiana t
8	21	28.4	11	6 Q9GL48	Q9gl48 sus scrofa
9	21	28.4	13	4 Q3UDC5	Q3udc5 homo sapien
10	21	28.4	13	10 Q43174	Q43174 solanum tub
11	21	28.4	13	12 P90442	P90442 spodoptera
12	20	27.0	10	2 Q8RJF1	Q8rjf1 pseudomonas
13	20	27.0	12	5 Q61574	Q61574 osteragla
14	20	27.0	12	11 Q80XV4	Q80xv4 rattus sp.
15	20	27.0	12	11 Q64313	Q64313 rattus norv
16	20	27.0	13	12 Q67604	Q67604 squash leaf

## ALIGNMENTS

### RESULT 1

Q80W11 ID Q80W11 PRELIMINARY; PRT; 11 AA.  
AC Q80W11;  
DT 01-JUN-2003 (T-EMBLrel. 24, Created)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE NT-3 transcript A (Fragment).  
GN NT-3.  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95040015; PubMed=7952296;  
RA Leingartner A., Lindholm D.;  
RT "Two promoters direct transcription of the mouse NT-3 gene."  
RL Eur. J. Neurosci. 6:1149-1159(1994).  
DR EMBL; S75812; AAPJ1855.1; -.  
FT NON\_CODING  
SQ SEQUENCE 11 AA; 1348 MW; 2280047D0DCA777 CRC64;

Query Match 35.1%; Score 26; DB 11; Length 11;  
Best Local Similarity 44.4%; Pred. No. 1e+03; Mismatches 4; Indels 0; Gaps 0;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

### Qy 5 YRPPNAPIL 13

YRPPNAPIL 13  
: : : : :  
2 WQPPSARIM 10

### RESULT 2

Q3UE86 ID Q3UE86 PRELIMINARY; PRT; 10 AA.  
AC Q3UE86;  
DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

```

DE Collagen alpha 1(I) chain (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92042176; PubMed=1939261;
RA Hawkins J.R., Superfi-Furga A., Steinmann B., Dalglish R.;
RT "A 9-base pair deletion in COL1A1 in a lethal variant of osteogenesis
RT imperfecta";
RL J. Biol. Chem. 266:22370-22374(1991).
DR EMBL; S66556; AAB20361.1; -.
DR GO; GO:0005584; C:collagen type I; NAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
DR GO; GO:0007155; P:cell adhesion; NAS.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 777 MW; 2D20F6D8676DD867 CRC64;

Query Match 33.8%; Score 25; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPNAP 11
DB 2 PPGAP 6

RESULT 3
Q9PSW5 PRELIMINARY; PRT; 12 AA.
AC Q9PSW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE I kappa B-alpha (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96125200; PubMed=9543172;
RA Krishnan V.A., Schazle J.D., Hinojos C.M., Bose H.R. Jr.;
RT "Structure and regulation of the gene encoding avian inhibitor of
RT nuclear factor kappa B-alpha.";
RL Gene 166:261-266(1995).
DR EMBL; L27342; AAA92641.1; -.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1276 MW; E584F64824C77401 CRC64;

Query Match 31.1%; Score 23; DB 13; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 AYRPPNAP 11
DB 4 AHRPAEPP 11

RESULT 4
Q9UCS8 PRELIMINARY; PRT; 9 AA.
AC Q9UCS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92075598; PubMed=1742316;
RA Ehnholm C., Bozas S.E., Tenkanen H., Kirszbaum L., Metso J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40.40
RT protein of human blood are different proteins which both bind to
RT apolipoprotein A-I.";
RL Biochim. Biophys. Acta 1086:255-260(1991).
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005319; F:lipid transporter activity; NAS.
DR GO; GO:0008203; P:cholesterol metabolism; ISS.
DR GO; GO:0008669; P:lipid transport; ISS.
FT NON_TER 1
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match 29.7%; Score 22; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPNAP 11
DB 3 PPGSP 7

RESULT 5
P82429 PRELIMINARY; PRT; 9 AA.
AC P82429;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 44 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RA STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 986 MW; C22CCAADC6C77776 CRC64;

Query Match 29.7%; Score 22; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 RPPNAPIL 13
DB 2 QPPQADFL 9

RESULT 6
Q9PRJ4 PRELIMINARY; PRT; 9 AA.
AC Q9PRJ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Bradykinin.

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OS Lepisosteus osseus (Long-nosed gar), and
OS Amla calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus.
OX NCBI_TaxID=34771, 7924;
RN [1] SEQUENCE.
RX MEDLINE=95389361; PubMed=7651903;
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar.";
RL Peptides 16:485-489 (1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;

Query Match 29.7%; Score 22; DB 13; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
Db |||:|
2 PPGWSP 7

RESULT 7
P82441 PRELIMINARY; PRT; 12 AA.
AC P82441
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 26 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1] SEQUENCE.
RC STRAIN=cv. PETIT HAVANA.
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON TER 12
SQ SEQUENCE 12 AA; 1234 MW; 340012240872C9D7 CRC64;

Query Match 29.1%; Score 21.5; DB 10; Length 12;
Best Local Similarity 41.7%; Pred. No. 5.6e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 1 TPPAYRPENAPI 12
Db |||:|:|
1 SPFA---PFVPV 9

RESULT 8
Q9GL48 PRELIMINARY; PRT; 11 AA.
AC Q9GL48
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE G protein-coupled receptor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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OX NCBI_TaxID=9823;
RN [1] SEQUENCE FROM N.A.
RA Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson L.,
RA Heslan J.-M., Soullieu J.-P., Charreau B.;
RT "Alternative double screening for differentially expressed genes by
RT modified RNA differential display and semi-quantitative Reverse
RT Northern blot.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF319662; AAC33870.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
FT NON TER 1
SQ SEQUENCE 11 AA; 1298 MW; 822261F10861BB41 CRC64;

Query Match 28.4%; Score 21; DB 6; Length 11;
Best Local Similarity 75.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPAY 5
Db |||:|
2 PPTY 5

RESULT 9
Q9UDC6 PRELIMINARY; PRT; 13 AA.
AC Q9UDC6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ENDOTHELIUM-derived RELATING factor, nitric oxide synthase
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RX MEDLINE=93054573; PubMed=1385404;
RA Janssens S.P., Simouchi A., Quertemous T., Bloch D.B., Bloch K.D.;
RT "Cloning and expression of a cDNA encoding human endothelium-derived
RT relating factor/nitric oxide synthase.";
RL J. Biol. Chem. 267:22694-22694(1992).
FT NON TER 13
SQ SEQUENCE 13 AA; 1390 MW; 3231B6DFEC7BB867 CRC64;

Query Match 28.4%; Score 21; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 7.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 4 AYRPP---NAP 11
Db |||:|:|
2 AFDPPGSDTNSP 13

RESULT 10
Q43174 PRELIMINARY; PRT; 13 AA.
AC Q43174
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-fructofuranosidase (EC 3.2.1.26) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=cv. Cara;

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RX MEDLINE=96279736; PubMed=8710506;
RA Bournay A.S., Hedley P.E., Maddison A., Waugh R., Machray G.C.;
RT "Exon skipping induced by cold stress in a potato invertase gene
transcript."
RL Nucleic Acids Res. 24:2347-2351(1996).
DR EMBL; X95821; CAA65087.1; -.
DR GO; GO:0004564; P:beta-fructofuranosidase activity; IEA.
DR GO; GO:0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
KW Glycosidase; Hydrolase.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1541 MW; 1B3053E7384C6874 CRC64;

Query Match 28.4%; Score 21; DB 10; Length 13;
Best Local Similarity 60.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PNAPI 12
DB 5 PNGPM 9

RESULT 11
P90442 ID P90442 PRELIMINARY; PRT; 13 AA.
AC P90442;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyhedrin (Fragment).
OS Spodoptera littoralis nuclear polyhedrosis virus (SNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10456;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E15; PubMed=9155969;
RA Faktor O., Tolster-Achituv M., Nachum O.;
RT "Enhancer element, repetitive sequences and gene organization in an 8-
kbp region containing the polyhedrin gene of the Spodoptera littoralis
nucleopolyhedrovirus."
RL Arch. Virol. 142:1-15(1997).
DR EMBL; X99711; CAA68046.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001746; Polyhedrin.
DR Pfam; PF00738; Polyhedrin; 1.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1383 MW; 2B0CD62832655737 CRC64;

Query Match 28.4%; Score 21; DB 12; Length 13;
Best Local Similarity 80.0%; Pred. No. 7.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TPPAY 5
DB 9 TGPAY 13

RESULT 12
Q8RJF1 ID Q8RJF1 PRELIMINARY; PRT; 10 AA.
AC Q8RJF1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Porin-like protein (Fragment).
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=NC16-2, TC29-5, and TC97;
RC TRANSDON=TN5041A1, TN5041B, and TN5041D1;
RA Kholodil G.Y., Gorlenko Z.M., Mindlin S.Z., Nikiforov V.G.;
RT "Distribution of distinct microvariants of TN5041 in environmental
bacteria."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ422128; CAD19527.1; -.
DR EMBL; AJ422129; CAD19528.1; -.
DR EMBL; AJ422130; CAD19529.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 23C47E7401F5A417 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPAYRP 7
DB 3 PRSHRP 8

RESULT 13
O61574 ID O61574 PRELIMINARY; PRT; 12 AA.
AC O61574;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Ostertagia ostertagi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
OX NCBI_TaxID=6317;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20233682; PubMed=10769181;
RA Moore J., Tetley L., Devaney E.;
RT "Identification of abundant mRNAs from the third stage larvae of the
parasitic nematode, Ostertagia ostertagi."
RL Biochem. J. 347:763-770(2000).
DR EMBL; AF052049; AAC06297.1; -.
KW Hypothetical protein.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1369 MW; C6FF867C1CA776C6 CRC64;

Query Match 27.0%; Score 20; DB 5; Length 12;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPAYRP 7
DB 2 PPXQP 7

RESULT 14
Q80XV4 ID Q80XV4 PRELIMINARY; PRT; 12 AA.
AC Q80XV4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orf4.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94012815; PubMed=8408077;
RA Rao S.M., Howells R.D.;
RT "cis-acting elements in the 5'-untranslated region of rat testis
proenkephalin mRNA regulate translation of the precursor protein."

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RL J. Biol. Chem. 268:22164-22169(1993).

DR EMBL; S66180; AAF13974.1; -.

SQ SEQUENCE 12 AA; 1436 MW; D33C6D2A83B36776 CRC64;

#### Query Match

27.0%; Score 20; DB 11; Length 12;

Best Local Similarity 60.0%; Pred. No. 9.7e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PPNAP 11

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Db 2 PPRQP 6

#### RESULT 15

Q64313

AC Q64313 PRELIMINARY; PRT; 12 AA.

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN ENK.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_taxID=10116;

EN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Fisher 344; TISSUE=Striatum;

RX MEDLINE=90066445; PubMed=2573832;

RA Garrett J.E., Collard M.W., Douglass J.O.;

RT "Translational control of germ cell-expressed mRNA imposed by

alternative splicing: opioid peptide gene expression in rat testis."

RL Mol. Cell. Biol. 9:4381-4389(1989).

DR EMBL; K02805; AAA60733.1; -.

KW Hypothetical protein.

SQ SEQUENCE 12 AA; 1436 MW; D33C6D2A83B36776 CRC64;

#### Query Match

27.0%; Score 20; DB 11; Length 12;

Best Local Similarity 60.0%; Pred. No. 9.7e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 PPNAP 11

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Db 2 PPRQP 6

Search completed: August 9, 2004, 18:35:43.

Job time : 35 secs

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